



[illegible]

QY	181	FEIHVPGCTCVLPKRSV	197
Db	181	efihvpgctcvlpkrsv	197
RESULT	2		
AA07602			
ID.	AA07602	standard; Protein; 197 AA.	
AC	AA07602;		
DT	07-NOV-2000	(first entry)	
XX			
DE	A human interleukin (IL) 171 polypeptide.		
XX			
KW	Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;		
XX	IL-177; IL-171; cell proliferation; cancer.		
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	Peptide	1..17	
FT		/note= "signal peptide"	
FT	Protein	18..197	
FT		/note= "mature protein"	
XX			
PN	MO200042188-A2.		
PD	20-JUL-2000.		
XX			
PF	10-JAN-2000; 2000WO-US00006.		
XX			
PR	11-JAN-1999; 99US-0228822.		
XX			
PA	(SCHE ) SCHERING CORP.		
XX			
PI	Gorman DM, Bazan JF, Kastelein RA;		
XX	WPI; 2000-466130/40.		
DR	N-PSDB; AAA58991.		
XX			
PT	New isolated polynucleotide encoding a mammalian interleukin-17 like		
XX	protein used to identify genes for homologous proteins -		
XX			
XX	Disclosure: Page 20-21; 11pp; English.		
CC	The present sequence represents an interleukin-171 (IL-171) polypeptide.		
CC	The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a		
CC	member of a new group of interleukins, IL-170 polypeptides. The members		
CC	comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170		
CC	or degenerative conditions. Antibodies can be used in diagnostic		
CC	methods to detect over production of IL-170 protein in cells or body		
CC	fluids.		
XX			
SQ	Sequence 197 AA;		
Query Match	100.0%; Score 1073; DB 21; Length 197;		
Best Local Similarity	100.0%; Pred. NO. 4.6e-109;		
Matches 197:	Conservative 0; Mismatches 0; Indels 0; Gaps 0		
QY	1	MTLPLGLFLFWLHTCLAHHPSTSLGHRPHSHGTPhCYSAEELPLDGAAPHLLARGAKMGO	60
Db	1	mlllpgllflfclwhcbclahndpsltgphnshgtphncysaeelpisqdephllargakwq	60
QY	61	ALPALVSSLEDAASHGRHERPSATTCPPVLPEEVYLEADTHQRNSISPMRYAVTDDEDRY	120
Db	61	alpalvaslleaasrgrherpsattgcgvvlrpeevleadtqgrsispmryvtvdteddy	120
QY	121	POKIAFAACLCRCIGDATGRTALNSVRILQSILLVRRRCSRDSGSGLPTRGAFAPHT	180

Db 121 pqlaiaecicgcidartgretaalnsrvllgslvlrrpcsdgsglprpgafafnt 180  
 QY 181 EFIRHPVGCTCVLPFRSV 197  
 |||||  
 Db 181 efihvpvgctcvlprsv 197

## RESULT 3

AAB07684  
 ID AAB07684 standard; Protein; 197 AA.

AC AAB07684;  
 DT 07-NOV-2000 (first entry)

DE A human interleukin-171 polypeptide.

KW Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;  
 IL-174; IL-176; IL-177; cell proliferation; cancer.

OS Homo sapiens.

FT Key Location/Qualifiers  
 FT Peptide 1..17

FT Protein /note= "signal peptide"  
 18..197

FT Modified-site /note= "mature protein"  
 55..57  
 FT /note= "putative glycosylation site"

PN WO200042187-A1.

PD 20-JUL-2000.

PE 10-JAN-2000; 2000WO-US00005.

PR 11-JAN-1999; 99US-0229402.

PA (SCHE ) SCHERING CORP.

PI Gorman DM, Bazan JF, Kastelein RA;

DR WPI: 2000-476060/41.  
 N-PSDB: AAA59149.

PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
 Interleukin-171 (IL-171), useful for recombinant production of IL-171  
 PT which can be used for treating conditions associated with abnormal  
 PT physiology or development

PS Claim 11; Page 10-11; 111pp; English.

CC The present sequence represents an interleukin (IL)-171 polypeptide.  
 CC It is a mammalian homologue of the cytokine designated CTLA-8 (also  
 CC referred to as IL-17). The specification also describes homologues  
 CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
 CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
 CC cDNA molecules which code for related or homologous proteins. The  
 CC IL-171 protein, antibodies against IL-171, and compounds which have  
 CC binding affinity to IL-171 are useful in treatment of conditions  
 CC associated with abnormal physiology or development, including abnormal  
 CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
 CC The IL-171 protein can be used in kits and assay methods for identifying  
 CC compounds that selectively bind to IL-171.

XX Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;

Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLIPGLLFTWLHTCLAHNDPSLRGHPHSHTGPHCSAEELPLGAPPHLLARGAKWQ 60

Db |||||  
 1 mtlipglflftwhtclahndpslrghphshgphcsaeelpigqaphllargakwq 60  
 QY 61 ALPVALVSSLEASHRGHREPRSATTOCPVLPREEVLEADTHORSTSPRYRVDTDEDR 120  
 |||||  
 Db 61 alpvalvssleashrghrerpsatcqvlpreevleadtqrsisprryrvdtdedry 120  
 QY 121 POKLAFECICRCIDARTGRETAAALNSVRLQSLVLRRRPCSRDPGSGLPFGAPAFHT 180  
 |||||  
 Db 121 pqlaiaecicgcidartgretaalnsrvllgslvlrrpcsdgsglprpgafafnt 180  
 QY 181 EFIRHPVGCTCVLPFRSV 197  
 |||||  
 Db 181 efihvpvgctcvlprsv 197

## RESULT 4

AAV92238  
 ID AAV92238 standard; Protein; 197 AA.

AC AAV92238;  
 DT 10-AUG-2000 (first entry)

DE Human interleukin-17 (IL-17) homologue.

KW Interleukin 17; IL-17; haematopoiesis; chemotherapy; cytostatic;  
 antianemic; cardiac; hemostatic; anti-inflammatory; anti-HIV.

OS Homo sapiens.

FT Key Location/Qualifiers  
 FT Peptide 1..18

FT Protein /label= signal\_peptide  
 19..197  
 FT /label= mature\_protein

PN WO200020593-A1.

PD 13-APR-2000.

PE 30-SEP-1999; 99WO-US22678.

PR 02-OCT-1998; 98US-0102883.

PR 01-DEC-1998; 98US-0110405.

PR 11-JUN-1999; 99US-0138910.

PA (ELIL ) LILLY & CO ERI.

PI Glasebrook AL, Su EW, Wei J, Liu L;

DR WPI: 2000-303778/26.

DR N-PSDB: AAA09153.

PT Nucleic acid encoding an interleukin-17 (IL-17) homologue polypeptide  
 PT which enhances hematopoiesis, useful for treating e.g. anemia,  
 PT thrombocytopenia, viral and bacterial infections

PS Claim 16; Page 92-93; 111pp; English.

CC Interleukin 17 (IL-17) stimulates hematopoiesis and production of  
 CC neutrophils, granulocytes, or platelets, this may be useful during  
 CC chemotherapy. IL-17 homologues have at least one activity selected  
 CC from induction of cytotoxic T cells, induction of lymphokine-activated  
 CC killer cell proliferation or a B or T cell stimulation. The IL-17  
 CC homologue may also be used to treat viral or bacterial infections.  
 CC immune related diseases, anemia, leukemia, thrombocytopenia, uremia,  
 CC Von Willebrand disease, postoperative cardiovascular dysfunction,  
 CC treatment of AIDS (acquired immune deficiency syndrome)-related bone  
 CC marrow failure, and inflammatory diseases of the gastrointestinal  
 CC system, joints, and lungs.

XX Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPGLLFTWLHTCLAHNDPSLRGPHSGTPHCYSAEELPLGQAPPHILARGAKWGQ 60  
 Db 1 mtlpgllftwlhtclahndpslrghpshtgphcsaeelpgqapphilargakwgq 60

QY 61 ALPAVALSSLEASHRGHERPSATTOCPVLRPEVLEADTHORSISPMWRVDTDEDRY 120  
 Db 61 alpavalsleashrgherpsatlcgvlrpeevleadthgrsispwryvdtde dry 120

QY 121 POKLAFAECRCRCIDARTGRERALNSVRLQSLVLRRRPCSDGSGLPFGAFAFHT 180  
 Db 121 pklafaeclrcrcidartgreretaalnsvrlqslvlrrrrpcsdgsglptgafafht 180

QY 181 EFHVPVGCCTCVLPFRSV 197  
 Db 181 efhvpvgctcvlprsv 197

RESULT 5  
 AAY44460  
 ID AAY44460 standard; Protein; 197 AA.  
 AC AAY44460;  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE Human Interleukin 17C, PRO1122 polypeptide.  
 XX  
 KW Interleukin; IL-17C; PRO1122 polypeptide; clone DNA62377-1381-1; UN0561;  
 KW cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;  
 KW hybridisation probe; antagonist; degenerative cartilaginous disorder;  
 KW agonist; diagnose; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label= Signal\_Peptide  
 FT 19..197  
 FT /label= Mature\_IL-17C\_polypeptide  
 FT /note= "Used to treat degenerative cartilaginous disorder"  
 FT Misc-difference 109  
 FT /note= "Conserved Trp residue"  
 FT Misc-difference 129  
 FT /note= "Conserved Cys residue"  
 FT Misc-difference 134  
 FT /note= "Conserved Cys residue"  
 FT Misc-difference 163  
 FT /note= "Conserved Cys residue"  
 FT Misc-difference 189  
 FT /note= "Conserved Cys residue"  
 FT Misc-difference 191  
 FT /note= "Conserved Cys residue"  
 FT /note= "Conserved Cys residue"  
 PN W09960127-A2.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 14-MAY-1999; 99MO-US10733.  
 XX  
 PR 15-MAY-1998; 98US-0085579.  
 PR 23-DEC-1998; 98US-0113621.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI.  
 XX

DR WPI: 2000-116314/10.  
 DR N-PSDB; AAZ29728.  
 XX  
 FT New polypeptides designated PRO1031 and PRO1122 used to treat a  
 PT degenerative cartilaginous disorder -  
 XX  
 PS Claim 23; Fig 3; 141pp; English.  
 XX  
 CC The present sequence is the human PRO1122 polypeptide, also referred to  
 CC as UN0561, and as Interleukin-17C (IL-17C), encoded by  
 CC clone DNA62377-1381-1. This sequence has identity with the  
 CC cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8)  
 CC and has leucine zipper pattern. PRO1122 is expressed in pancreas, small  
 CC intestine, stomach and testis also. It shares about 26-28% amino acid  
 CC identity with IL-17 and IL-17B. The entire coding region of IL-17C can  
 CC be used as hybridisation probe. The PRO1122 polypeptide, agonist or  
 CC antagonist, is used to diagnose and treat a degenerative cartilaginous  
 CC disorder.  
 XX  
 SQ Sequence 197 AA;

Query Match 100.0%; Score 1073; DB 21; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPGLLFTWLHTCLAHNDPSLRGPHSGTPHCYSAEELPLGQAPPHILARGAKWGQ 60  
 Db 1 mtlpgllftwlhtclahndpslrghpshtgphcsaeelpgqapphilargakwgq 60

QY 61 ALPAVALSSLEASHRGHERPSATTOCPVLRPEVLEADTHORSISPMWRVDTDEDRY 120  
 Db 61 alpavalsleashrgherpsatlcgvlrpeevleadthgrsispwryvdtde dry 120

QY 121 POKLAFAECRCRCIDARTGRERALNSVRLQSLVLRRRPCSDGSGLPFGAFAFHT 180  
 Db 121 pklafaeclrcrcidartgreretaalnsvrlqslvlrrrrpcsdgsglptgafafht 180

QY 181 EFHVPVGCCTCVLPFRSV 197  
 Db 181 efhvpvgctcvlprsv 197

RESULT 6  
 AAY53892  
 ID AAY53892 standard; Protein; 197 AA.  
 AC AAY53892;  
 XX  
 DT 13-MAR-2000 (first entry)  
 XX  
 DE Amino acid sequence of human Interleukin-21.  
 XX  
 KW Human; Interleukin-22; IL-22; IL-21; immune system disorder;  
 KW immune cell chemotaxis; haematopoietic cell disorder;  
 KW haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;  
 KW respiratory problem; organ rejection; graft-versus-host disease; GVHD;  
 KW inflammation; hyperproliferative disorder; tissue regeneration;  
 KW embryonic stem cell differentiation; embryonic stem cell proliferation;  
 KW haematopoietic lineage; allergic asthma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /note= "signal peptide"  
 FT 34..40  
 FT /note= "conserved domain V"  
 FT 63..68  
 FT /note= "conserved domain VI"  
 FT 104..109  
 FT /note= "conserved domain VII"  
 FT 113..121  
 FT Domain



CC differentiation or mobilization of immune cells, disorders of  
 CC hematopoietic cells (e.g. leukaemia, human immunodeficiency virus (HIV)  
 CC infection, anemia, thrombocytopenia), autoimmune disorders (e.g. Grave's  
 CC disease, systemic lupus erythematosus, ophthalmia), graft versus host  
 CC disease, inflammation, hyperproliferative disorders, or infectious  
 CC diseases. The polypeptides are useful for generating antibodies, which  
 CC can be used to treat, inhibit or prevent diseases or conditions  
 CC associated with aberrant expression and/or activity of IL-21 or IL-22.  
 CC The present sequence represents the amino acid sequence of human IL-21.  
 CC  
 XX Sequence 197 AA:

Query Match 100.0%; Score 1073; DB 22; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTLPGLLFTWLHTCLAHHPDRLRGHSHGTPHCYSAEELPLGQAPPHILARAKMGQ 60  
 DB 1 mtlpgllftwlhtclahdpdrlrgshgtpchysaeelpigqapphillargakwgq 60  
 OY 61 ALPVALVSLLEASHRGHREPSATTQCPVLRPEEVLADTHORSISPMRYVTDDEKRY 120  
 DB 61 alpvalvslleaashrghepstattpcvlrpeeleadthqrsispwryvtdedry 120  
 OY 121 POKLAFAECLRCGIDARIGRETAALNSVRLQSLVLRPPCRSGSGLTPGAFAPHT 180  
 DB 121 pqklafaeclrcgidartgretaalnsvrlqslvlrrpcsrdsqsltpgafafht 180  
 OY 181 EFHVPVGCVCVLRPSV 197  
 DB 181 efhvpvgcvcvlpvsv 197

RESULT 8  
 AAU29247  
 ID AAU29247 standard; Protein: 197 AA.

AC AAU29247;  
 DT 18-DEC-2001 (first entry)  
 XX Human PRO polypeptide sequence #224.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

OS Homo sapiens.

PN WO200168848-A2.

PD 20-SEP-2001.

PF 28-FEB-2001; 2001WO-US06520.

XX 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 03-MAR-2000; 2000US-187202P.  
 PR 06-MAR-2000; 2000US-186968P.  
 PR 14-MAR-2000; 2000US-189330P.  
 PR 14-MAR-2000; 2000US-189328P.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000US-190828P.  
 PR 21-MAR-2000; 2000US-191007P.  
 PR 21-MAR-2000; 2000US-191048P.  
 PR 21-MAR-2000; 2000US-191314P.  
 PR 28-MAR-2000; 2000US-192655P.  
 PR 29-MAR-2000; 2000US-193032P.  
 PR 30-MAR-2000; 2000US-193053P.  
 PR 04-APR-2000; 2000WO-US08439.  
 PR 04-APR-2000; 2000US-194449P.

PR 04-APR-2000; 2000US-194647P.  
 PR 11-APR-2000; 2000US-195975P.  
 PR 11-APR-2000; 2000US-196000P.  
 PR 11-APR-2000; 2000US-196187P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 11-APR-2000; 2000US-196820P.  
 PR 18-APR-2000; 2000US-198121P.  
 PR 18-APR-2000; 2000US-198585P.  
 PR 25-APR-2000; 2000US-199397P.  
 PR 25-APR-2000; 2000US-199550P.  
 PR 25-APR-2000; 2000US-199654P.  
 PR 03-MAY-2000; 2000US-201516P.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 05-JUN-2000; 2000US-209832P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 22-AUG-2000; 2000WO-US44848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.

PA (GENTH) GENENTECH INC.

PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WL, Zhang Z;

DR WPI: 2001-602746/68.

DR N-PSDB; AAS46148.

PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds

XX Claim 11; Fig 448; 774pp; English.

XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.  
 XX

SQ Sequence 197 AA:

Query Match 100.0%; Score 1073; DB 22; Length 197;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTLPGLLFTWLHTCLAHHPDRLRGHSHGTPHCYSAEELPLGQAPPHILARAKMGQ 60  
 DB 1 mtlpgllftwlhtclahdpdrlrgshgtpchysaeelpigqapphillargakwgq 60  
 OY 61 ALPVALVSLLEASHRGHREPSATTQCPVLRPEEVLADTHORSISPMRYVTDDEKRY 120  
 DB 61 alpvalvslleaashrghepstattpcvlrpeeleadthqrsispwryvtdedry 120  
 OY 121 POKLAFAECLRCGIDARIGRETAALNSVRLQSLVLRPPCRSGSGLTPGAFAPHT 180  
 DB 121 pqklafaeclrcgidartgretaalnsvrlqslvlrrpcsrdsqsltpgafafht 180

QY 181 EFHVPVGTCTVLPVRSV 197  
 PT |-----|  
 DB 181 efhvpvgtctvlpvrsv 197

RESULT 9  
 AAU04951  
 ID AAU04951 standard; Protein; 197 AA.  
 XX  
 AC AAU04951;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human Interleukin 17C ligand, IL-17C.  
 XX  
 KW Human; Interleukin-17C ligand; IL-17C; agonist; antagonist;  
 KW PRO1122; DNA 62377-1381-1; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;  
 KW allergic disease; asthma; demyelinating disease;  
 KW degenerative cartilaginous disorder; transplantation associated disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..18  
 FT /label= Signal\_peptide  
 FT 3..25  
 FT /note= "Leucine zipper pattern"  
 FT 19..197  
 FT /label= Mature\_IL\_17C  
 FT 32..38  
 FT /note= "N-myristoylation site"  
 FT 55..61  
 FT /note= "N-myristoylation site"  
 FT 99..125  
 FT /note= "Region homologous to IL-17"  
 FT 112..121  
 FT /note= "Tyrosine kinase phosphorylation site"  
 FT 133..139  
 FT /note= "N-myristoylation site"  
 XX  
 PN WO200146420-A2.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PE 20-DEC-2000; 2000WO-US34956.  
 XX  
 PR 23-DEC-1999; 99US-0172096.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 11-JAN-2000; 2000US-0175481.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 21-MAR-2000; 2000US-0191007.  
 PR 02-JUN-2000; 2000WO-US07532.  
 PR 22-JUN-2000; 2000US-0213087.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 24-OCT-2000; 2000US-0242837.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-0253646.  
 PR 01-DEC-2000; 2000WO-US32678.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;  
 PI Gurey AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandalen RL;  
 PI Watanabe CK, Williams PM, Wood WL, Yansura DG;  
 XX WPI: 2001-451708/48.  
 DR N-PSDB: AAS09510.  
 XX

PT Novel PRO polypeptides homologous to interleukin-17, useful for the  
 PT diagnosis and treatment of immune related disease e.g. rheumatoid  
 PT arthritis and diabetes  
 XX  
 PS Claim 10; Fig 4; 186pp; English.  
 XX  
 CC The sequence is PRO1122 which is the human Interleukin 17C ligand,  
 CC IL-17C, encoded by DNA 62377-1381-1. A composition  
 CC containing ant/agonists to the PRO polypeptides or individual components  
 CC are useful for treating a mammal with an immune related disease, e.g.  
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, a  
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin  
 CC disease, contact dermatitis, an allergic disease e.g. food  
 CC hypersensitivity, asthma, a transplantation associated disease, or a  
 CC chronic inflammatory demyelinating polyneuropathy. Treating a  
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or  
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous  
 CC examples of the diseases and disorders are given in the specification.  
 XX  
 SQ Sequence 197 AA;  
 XX

Query Match 100.0%; Score 1073; DB 22; Length 197;  
 Best Local Similarity 100.0%; Pred No. 4.6e-109;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLPLLEFLTWLHTCLAHSDPSLRGPHSGTSPHCYSAEELPLGAPPHLARGAKWQ 60  
 DB 1 mtlplllflftwhtclahdpslrgphshgphcysaeelplgapphlargakwq 60

QY 61 ALPVAVSSLEAASHGRHSPSATTCQVLPREEVLEADTHQRSISPMARYRDTEDRY 120  
 DB 61 alpvalvssleaashgrhspattpcqlrpeevleadtqrsispmryrvtledry 120

QY 121 POKLAFECRCRCIDARCFRTAALNSVRLQSLVLRPPSRGSGPTGAFAR 180  
 DB 121 pqlafecrcrcidarcfretaalnsvrlqslvlrrppsrsgsgptgafarf 180

QY 181 EFHVPVGTCTVLPVRSV 197  
 DB 181 efhvpvgtctvlpvrsv 197

RESULT 10  
 AA44485  
 ID AA44485 standard; Protein; 206 AA.  
 XX  
 AC AA44485;  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE Human Interleukin 17C with C-terminal Gly(His)8 tag, IL-17C.his.  
 XX  
 KW Interleukin; IL-17C.his; PRO1122 polypeptide; clone DNA62377-1381-1;  
 KW immunoprecipitation; IL-17 receptor extracellular domain; IL-17R ECD;  
 KW cytokine IL-17; hybridisation probe; antagonist; Gly(His)8 tag; agonist;  
 KW degenerative cartilaginous disorder; diagnosis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..18  
 FT /label= Signal\_peptide  
 FT 19..197  
 FT /label= Mature\_IL-17C.polypeptide  
 FT /note= "Used to treat degenerative cartilaginous  
 FT disorder"  
 FT Misc-difference 109  
 FT /note= "Conserved Trp residue"

XX	Human Interleukin 17C-IgG1 Fc fusion protein, hIL-17C.fc.
KM	Interleukin; IL-17C.fc; fusion protein; PRO1122 polypeptide; cytokine;
KW	human IgG1; fluorescence-activated cell sorter analysis; FACS;
KM	Tumour Necrosis Factor-alpha; TNF-alpha; leukemic monocyte; TNP-1 cell
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..18
FT	/label= Signal_peptide
FT	Protein
FT	19..197
FT	/label= Mature_IL-17C-polypeptide
FT	/note= "used to treat degenerative cartilaginous disorder"
FT	Misc-difference
FT	109
FT	/note= "Conserved Trp residue"
FT	Misc-difference
FT	129
FT	/note= "Conserved Cys residue"
FT	Misc-difference
FT	134
FT	/note= "Conserved Cys residue"
FT	Misc-difference
FT	163
FT	/note= "Conserved Cys residue"
FT	Misc-difference
FT	189
FT	/note= "Conserved Cys residue"
FT	Misc-difference
FT	191
FT	/note= "Conserved Cys residue"
FT	Region
FT	197..425
FT	/note= "Sequence derived from Fc region of human IgG1"
PN	MO9960127-A2.
XX	
PD	25-NOV-1999.
XX	
PF	14-MAY-1999; 99WO-US10733.
XX	
PR	15-MAY-1998; 98US-0085579.
PR	23-DEC-1998; 98US-0113621.
PA	(GETH ) GENENTECH INC.
XX	
XX	Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WI,
XX	

PT	New polypeptides designated PRO1031 and PRO1122 used to treat a
PT	degenerative cartilaginous disorder -
PS	Example 12; Page 129-130; 141pp; English.
PX	
XX	
CC	The present sequence is the human IL-17C .fc fusion protein, derived from
CC	PRO1122 polypeptide and the FC region of human IgG1. The cytokine IL-17C
CC	can be used to induce the release of TNF-alpha from human leukemic
CC	monocytic, THP-1 cells. The fusion protein, IL-17C .fc is used to identify
CC	the binding of IL-17C to THP-1 cells, using fluorescence-activated cell
CC	sorter analysis (FACS).
SQ	Sequence      425 AA;
Query Match	100.0%; Score 1073; DB 21; Length 425;
Best Local Similarity	100.0%; Prid. No. 1.3e-108;
Matches 197; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MTLLPGLELFTWLTATCLAHHPDSLRGHSHSGTFCNCSAEELPLGAOPPHILARGAKMGQ 60
Dd	1 mtlpgllflftwltatclahhpdslrghshsgtfcncsaeeelpgggaaphlllrrgawkq 60
QY	61 ALPALVSSLEASHRGRHERPSATQCPLVPREEVEADTHORSISPMRYRVDTDEERY 120
Dd	61 alpvalssleashrgrherpsatqcplvpreeveadthorsispmryrvdtdeery 120
QY	121 PKLAFAECLRCGCIDARTGRETAALNSVRLLQSLLVLRPPCSRDSGSLTPFGAFAMHT 180



Db 121 pklafaelcrgcdartgretalaansvrlqslvlrrpcsrdsqslpqpafatnf 180  
 OY 181 EFHVPVGTCTVLPKRSV 197  
 Db 181 efthvpgctcvlpkrsv 197

## RESULT 12

AAE08676  
 ID AAE08676 standard: Protein; 227 AA.

XX AAE08676;

DT 15-NOV-2001 (first entry)

XX Human Interleukin (IL)-17 like protein.

XX Human; Interleukin; IL-17 like protein; rheumatic disease; gene therapy;

KW multiple sclerosis; graft versus host disease; inflammatory disease;

KM asthma; autoimmune disease; allergy; graft rejection; bone destruction;

KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;

KM neuroprotective; antirheumatic; antiallergic.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 5..48

XX /label= Signal\_peptide

XX 49..227

XX /label= Mature\_human\_IL-17\_like protein

XX WO200159120-A2.

XX 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US03916.

XX 08-FEB-2000; 2000US-0180864.

XX 27-NOV-2000; 2000US-0722920.

XX (AMGE-) AMGEN INC.

XX Jing S, Bass MB;

XX WPI: 2001-529841/58.

XX N-PSDB: AAD15291..

XX Novel interleukin-17 like polypeptides and nucleic acid molecules

XX encoding them useful for diagnosis, prevention and treatment of

XX inflammatory, autoimmune disease, allergies, asthma and organ or graft

XX rejection

XX Claim 14; Fig 1A; 117pp; English.

XX The present invention relates to interleukin (IL)-17 like polypeptides

XX and nucleic acids encoding them. IL-17 like protein is useful for

XX identifying binding partners, agonists and antagonists which can be used

XX for treating one or more diseases or disorders and for cloning IL-17

XX like receptors, using an expression cloning strategy. Radiolabelled or

CC gene therapy and for mapping the location of the IL-17 like gene and  
 CC related genes on chromosomes, as hybridisation probes in diagnostic  
 CC assays. Non-human animals in which the promoter for one or more of IL-17  
 CC like protein is either activated or inactivated are useful for drug  
 CC candidate screening. The present sequence is human IL-17 like protein.  
 XX  
 SQ Sequence 227 AA;

Query Match 99.1%; Score 1063; DB 22; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-108;  
 Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LPLGLFLTWLHTCLAHHPSSLRGHPHSHTGTPCYSAEELPLGQAPPHLLARGAKKGOAL 62

Db 33 lppglfltwlhtclahhpslrgphshgtpcyaaelpgqapphllargakkgal 92

OY 63 pVALVSSLEAASHRHGRHRSATTCQPVLRPEEVLADTHQRSISPMRYRVDTDEDRYQ 122

Db 93 pVALVSSLEAASHRHGRHRSATTCQPVLRPEEVLADTHQRSISPMRYRVDTDEDRYQ 152

OY 123 KLAFAACLCRGCTDARTGRETALNSVRLQSLVLRRRPCSDSGSLPPGAFARHTER 182

Db 153 klafaelcrgcdartgretalaansvrlqslvlrrpcsrdsqslpqpafatnf 212

OY 183 IHVPVGTCTVLPKRSV 197

Db 213 ihvpgctcvlpkrsv 227

## RESULT 13

AAE08680  
 ID AAE08680 standard: Protein; 227 AA.

XX AAE08680;

DT 15-NOV-2001 (first entry)

XX Human Interleukin (IL)-17 like protein mutant (Leu47Ile).

XX Human; Interleukin; IL-17 like protein; rheumatic disease; gene therapy;

KW multiple sclerosis; graft versus host disease; inflammatory disease;

KM asthma; autoimmune disease; allergy; graft rejection; bone destruction;

KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;

KM neuroprotective; antirheumatic; antiallergic; mutant; mutein.

OS Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 47

XX /note= "Wild-type Leu substituted with Ile"

XX WO200159120-A2.

XX 16-AUG-2001.

XX 07-FEB-2001; 2001WO-US03916.

XX 08-FEB-2000; 2000US-0180864.

XX 27-NOV-2000; 2000US-0722920.

XX (AMGE-) AMGEN INC.

XX Jing S, Bass MB;

XX WPI: 2001-529841/58.

XX Novel interleukin-17 like polypeptides and nucleic acid molecules

XX encoding them useful for diagnosis, prevention and treatment of

XX inflammatory, autoimmune disease, allergies, asthma and organ or graft

XX rejection

Claim 18; Page -; 117pp; English

XX PS Claim 18; Page -; 117pp; English.

CC The present invention relates to interleukin (IL)-17 like polypeptides  
CC and nucleic acids encoding them. IL-17 like protein is useful for  
CC identifying binding partners, agonists and antagonists which can be used  
CC for treating one or more diseases or disorders and for cloning IL-17  
CC like receptors, using an expression cloning strategy. Radiolabelled or  
CC affinity/activity-tagged IL-17 proteins are useful in binding assays to  
CC identify a cell type or cell line or tissue that express IL-17 like  
CC receptors. A radiolabelled or tagged IL-17 like protein is useful as an  
CC affinity ligand to identify and isolate from an expression library the  
CC subset of cells which express the IL-17 like receptors on their surface.  
CC IL-17 like protein, agonist and antagonist are useful for treating acute  
CC and chronic inflammation such as rheumatic diseases, graft versus host  
CC disease and multiple sclerosis. IL-17 like antagonists are useful for  
CC treating and preventing inflammatory disease, autoimmune disease,  
CC allergies, asthma and organ or graft rejection in a patient and also  
CC for inhibiting T cell proliferation and/or activation, in vivo B cell  
CC proliferation or immunoglobulin secretion, and for blocking the effects  
CC of IL-17 in inducing bone destruction. IL-17 like molecule is useful in  
CC gene therapy and for mapping the location of the IL-17 like gene and  
CC related genes on chromosomes, as hybridisation probes in diagnostic  
CC assays. Non-human animals, in which the promoter for one or more of IL-17  
CC like protein is either activated or inactivated are useful for drug  
CC candidate screening. The present sequence is human IL-17 like  
CC protein mutant (Leu471Ile).

CC Note: The present sequence is not shown in the specification, but is  
CC derived from the human IL-17 like protein referred to as SEQ ID NO:2  
CC (AAE08676), shown in figure 1A.

XX  
XX  
XX Sequence 227 AA.

50 Sequence 227 AA;.

Query Match	98.98;	Score 1061;	DB 22;	Length 227;
Best Local Similarity	99.58;	Pred. No. 1.1e-107;		
Matches 194;	Conservative	1;	Mismatches 0;	Indels 0;

QY	3	LLPQLLEFLTWHTATGLAHNDPSTLRGHPSHSGPHCYSAKEEPLGLGAPPHLLARAKMGQAL	62
Db	33	LLPQLLFLTWHTATGLAHNDPSTLRGHPSHSGPHCYSAKEEPLGLGAPPHLLARAKMGQAL	92
QY	63	PVALVSSLEAASHRGHRHRRPSATTQCQVLRPEEVLLEADTHQRSISPMRYRVDTEDEBTPQ	122
Db	93	pvalvssleaaashrgnrhrpsattqcqpylrpeeveelddthqrsispmyryvdtedctypq	155
QY	123	KLAFAELCRGCDIARFGRETFALINSVRLQSLVLLRRPDCSRDGSGLTPPGAFATFEEF	182
Db	153	klafaeclrcgcldarfgrctfalaainsvrlqlslvllrrpdcsrcdsgsltppgafatfctef	212
QY	183	IHHVPGCTCVLPKRSY	197
Db	213	ihhvpgctcvlpkrsy	227

RESULT	14
AAE08682	
ID	AAE08682 standard; Protein; 227 AA.
vv	

AC	AAE08682;	
XX		
DT	15-NOV-2001	(first entry)
ST		

DE	Human interleukin (IL)-17 like protein mutant (leu47Met).
XX	
KW	Human: interleukin; IL-17 like protein; rheumatic disease; gene therapy
KW	multiple sclerosis; graft versus host disease; inflammatory disease;
KW	asthma; autoimmune disease; allergy; graft rejection; bone destruction;
KW	drug screening; antiinflammatory; immunosuppressive; antiallumatic;
KW	neuroprotective; antirheumatic; antiallergic; mutant; mutagen
XX	

05	Homo sapiens
05	Synthetic.

FH	Key	Location/Qualifiers
ET	mic-a:46000000	47

	FT	XY
misc-difference	4	
FT		
XY		

Wild-type Leu substituted with Met

PN WO200159120-A2

PD 16-AUG-2001

PF - 07-FEB-2001; 2001WO-US03916.

PR 08-FEB-2000; 2000US-0180864.

PR 27-NOV-2000; 2000US-0722920.  
YY

PA (AMGE-) AMGEN INC  
VV

PI. Jing S, Bass MB;  
yy

DR WPI; 2001-529841/58  
xx

PT Novel interleukin-17 like polypeptides and nucleic acid molecules  
PT encoding them useful for diagnosis, prevention and treatment of  
PT inflammatory, autoimmune disease, allergies, asthma and organ or graft  
PT rejection -  
PT

PS	Claim 18; Page -; 117pp; English
VY	

The present invention relates to interleukin (IL)-17 like polypeptides and nucleic acids encoding them. IL-17 like protein is useful for identifying binding partners, agonists and antagonists which can be used for treating one or more diseases or disorders and for cloning IL-17 like receptors, using an expression cloning strategy. Radiolabelled or affinity/activity-tagged IL-17 proteins are useful in binding assays to identify a cell type or cell line or tissue that expresses IL-17 like receptors. A radiolabelled or tagged IL-17 like protein is useful as an affinity ligand to identify and isolate from an expression library the subset of cells which express the IL-17 like receptors on their surface. IL-17 like protein, agonist and antagonist are useful for treating acute and chronic inflammation such as rheumatic diseases, graft versus host disease and multiple sclerosis. IL-17 like antagonists are useful for treating and preventing inflammatory disease, autoimmune disease, allergies, asthma and organ or graft rejection in a patient and also for inhibiting T cell proliferation and/or activation, in vivo B cell proliferation or immunoglobulin secretion, and for blocking the effects of IL-17 in inducing bone destruction. IL-17 like molecule is useful in gene therapy and for mapping the location of the IL-17 like gene and related genes on chromosomes, as hybridisation probes in diagnostic assays. Non-human animals in which the promoter for one or more of IL-17 like protein is either activated or inactivated are useful for drug candidate screening. The present sequence is human IL-17 like protein mutant (Leu47Met).

Note: The present sequence is not shown in the specification, but is derived from the human IL-17 like protein referred to as SEQ ID NO:2 (AAE08676), shown in figure 1A.

50 Sequence 227 AA;

Query Match	98.9%	Score 1061;	DB 22;	Length 227;
Best Local Similarity	99.5%	Pred. No. 1.1e-107;		
Matches 194; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	3	LRPGLEETWLTHTLOLANHDDSLRGNHPSHSTPRHCYSAAEELPRGQARPHILLRGAKMGAL	62
Db	33	llpgllflftwlthtcmahhdpdsirgbrhsbgrtphcysaeelprlgqarphlllragatwgaal	92
QY	63	PVALVSSLEAASHRGHRRHSATTCQPVLRPEVYLEADTHQMSISPMKRYRVDTEDEKRPQ	122
Db	93	pvalvssleaaashrgtnerpsattgcqpvlrpeevleadtqrsisrpywtidtdedxyq	152
QY	123	KLAFAECICRCIDARFGRETAALNSVRLLOSLVLRRRPCRSDDSGLPRTGAARPTTFP	182
Db	153	klafaeccrcycidarfgrtaalnsvrllqslvlvrrpcrsdsglprrtgafathtef	212

Qy 183 IHPVGTCTVLP RSV 197  
 Db 213 IHPVGTCTVLP RSV 227

## RESULT 15

AAE08681  
 ID AAE08681 standard; Protein; 227 AA.

XX AC AAE08681;

XX DT 15-NOV-2001 (first entry)

XX DE Human interleukin (IL)-17 like protein mutant (Leu47Val).

XX KW Human; interleukin; IL-17 like protein; rheumatic disease; gene therapy;  
 KW multiple sclerosis; graft versus host disease; inflammatory disease;  
 KW asthma; autoimmune disease; allergy; graft rejection; bone destruction;  
 KW drug screening; antiinflammatory; immunosuppressive; antiasthmatic;  
 KW neuroprotective; antirheumatic; antiallergic; mutant; mutein.

XX OS Homo sapiens.  
 OS Synthetic.

XX XX Key Location/Qualifiers

FT Misc-difference 47 /note- "Wild-type Leu substituted with Val"

XX PN WO200159120-A2.

XX PD 16-AUG-2001.

XX PE 07-FEB-2001; 2001WO-US03916.

XX PR 08-FEB-2000; 2000US-0180864.

XX PR 27-NOV-2000; 2000US-0722920.

XX PA (AMGE-) AMGEN INC.

XX PI Jing S. Bass MB;

XX DR WPI; 2001-529841/58.

XX PT Novel interleukin-17 like polypeptides and nucleic acid molecules  
 PT encoding them useful for diagnosis, prevention and treatment of  
 PT inflammatory, autoimmune disease, allergies, asthma and organ or graft  
 PT rejection

XX PS Claim 18; Page -: 117pp; English.

XX CC The present invention relates to interleukin (IL)-17 like polypeptides  
 CC and nucleic acids encoding them. IL-17 like protein is useful for  
 CC identifying binding partners, agonists and antagonists which can be used  
 CC for treating one or more diseases or disorders and for cloning IL-17  
 CC like receptors, using an expression cloning strategy. Radiolabelled or  
 CC affinity/activity-tagged IL-17 proteins are useful in binding assays to  
 CC identify a cell type or cell line or tissue that expresses IL-17 like  
 CC receptors. A radiolabelled or tagged IL-17 like protein is useful as an  
 CC affinity ligand to identify and isolate from an expression library the  
 CC subset of cells which express the IL-17 like receptors on their surface.  
 CC IL-17 like protein, agonist and antagonist are useful for treating acute  
 CC and chronic inflammation such as rheumatic diseases, graft versus host  
 CC disease and multiple sclerosis. IL-17 like antagonists are useful for  
 CC treating and preventing inflammatory disease, autoimmune disease,  
 CC allergies, asthma and organ or graft rejection in a patient and also  
 CC for inhibiting T cell proliferation and/or activation, in vivo B cell  
 CC proliferation or immunoglobulin secretion, and for blocking the effects  
 CC of IL-17 in inducing bone destruction. IL-17 like molecule is useful in  
 CC gene therapy and for mapping the location of the IL-17 like gene and  
 CC related genes on chromosomes, as hybridisation probes in diagnostic  
 CC assays. Non-human animals in which the promoter for one or more of IL-17  
 CC like protein is either activated or inactivated are useful for drug  
 CC candidate screening. The present sequence is human IL-17 like

CC protein mutant (Leu47Val).  
 CC Note: The present sequence is not shown in the specification, but is  
 CC derived from the human IL-17 like protein referred to as SEQ ID NO:2  
 CC (AAE08676), shown in figure 1A.

XX SQ Sequence 227 AA;

Query Match 98.8%; Score 1060; DB 22; Length 227;  
 Best Local Similarity 99.5%; Pred. No. 1,5e-107;  
 Matches 194; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILPGILFTWLHTCLAHDPRLRGPHSHGPHCYSAEELPLGQAPPHLLARGAKWQAL 62  
 Db 33 IIPGILFTWLHTCLAHDPRLRGPHSHGPHCYSAEELPLGQAPPHLLARGAKWQAL 92  
 Qy 63 PVALVSSLEASHRGRHERPSATTCQPVLRPEVLEADTHQRSISPMWRVDTDED RY PQ 122  
 Db 93 pvalvssleashrgrherpsatcqpvlrpeevleadtqgsispwrvdtdedrypq 152  
 Qy 123 KIAFAECRCRCIDARTGRETALNSVRLQSLVLRPRPCRDGSGLPFGAFAPHTF 182  
 Db 153 KIAFAECRCRCIDARTGRETALNSVRLQSLVLRPRPCRDGSGLPFGAFAPHTF 212  
 Qy 183 IHPVGTCTVLP RSV 197  
 Db 213 IHPVGTCTVLP RSV 227

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2002, 23:54:32 ; Search time 1827.84 seconds  
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11986.872 Million cell updates/sec

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Perfect score: 1047  
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Scoring table:  
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Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 5: gb\_ov:\*
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- 8: gb\_pr:\*
- 9: gb\_ro:\*
- 10: gb\_sy:\*
- 11: gb\_sy:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
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- 16: em\_fun:\*
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- 18: em\_in:\*
- 19: em\_mu:\*
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- 21: em\_or:\*
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- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
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- 33: em\_htg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	1047	100.0	1047	6	AX180766	AX180766 Sequence
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3	1015.4	97.0	1078	9	AF142410	AF142410 Homo sapi
4	923.4	88.2	1177	6	AX223849	AX223849 Sequence
5	651	62.2	15689	2	AC103884	AC103884 Homo sapi
6	651	62.2	157090	2	AC022554	AC022554 Homo sapi
7	192.8	18.4	221647	10	AL591003	AL591003 Mouse DNA
8	69.8	6.7	125020	9	AF429315	AF429315 Homo sapi
9	61	5.8	125020	9	AF429315	AF429315 Homo sapi
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11	56.8	5.4	1734	6	AX180770	AX180770 Sequence
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14	53.8	5.1	644	6	AX253225	AX253225 Sequence
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18	53.6	5.1	204292	2	AP004071	AP004071 Oryza sat
19	53.4	5.1	114339	9	AC006409	AC006409 Homo sapi
20	53.4	5.1	209545	2	AC087848	AC087848 Homo sapi
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30	49.8	4.8	67213	2	AC024538	AC024538 Homo sapi
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33	48.2	4.7	144156	9	AL160276	AL160276 Human DNA
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38	47.4	4.5	2561	6	AX239605	AX239605 Sequence
39	47.4	4.5	136551	2	AC048354	AC048354 Homo sapi
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42	47.2	4.5	161981	2	AC103237	AC103237 Rattus no
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44	47	4.5	199008	2	AL645668	AL645668 Mus muscu
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## ALIGNMENTS

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DEFINITION	Sequence 3 from Patent WO0146420.
ACCESSION	AX180766
VERSION	AX180766.1 GI:15132617
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	Chen, J., Flyvareff, E., Fong, S., Goddard, A., Godowski, P. J., Grimaldi, C. J., Guirney, A. L., Li, H., Hillan, K. J., Tumas, D., van Lookeren, M., Vandlen, R. L., Watanabe, C. K., Williams, P. M., Wood, W. I., Il-17 and Il-17r homologous polypeptides and therapeutic uses thereof
TITLE	Patent: WO, 0146420-A 3 28-JUN-2001;
JOURNAL	Genentech, Inc. (US)
FEATURES	Location/Qualifiers
SOURCE	1..1047
	/organism="Homo sapiens"

BASE COUNT 177 a 381 c 280 g 209 t  
ORIGIN

Query Match 100.0%; Score 1047; DB 6; Length 1047;  
Best Local Similarity 100.0%; Pred. No. 7.4e-207;  
Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 cccggcctctgtttctgacctgtgcacacatgctgtgcccacatgacctctct 120
QY 121 cagggggagcccccaacagtcagagtaaccacactgtactgctgagaaactgccc 180
DB 121 cagggggagcccccaacagtcagagtaaccacactgtactgctgagaaactgccc 180
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## RESULT 2

AF152099

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

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AUTHORS

TITLE

JOURNAL

BASE COUNT

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ORIGIN

Query Match

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Best Local Similarity

100.0%; Pred. No. 7.4e-207;

Matches 1047; Conservative

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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1078)		
TITLE	Zhang, W., He, L., Wan, T., Yuan, Z., and Cao, X.		
JOURNAL	Novel human cytokine CX2 with homology to IL-17		
REFERENCE	2 (bases 1 to 1078)		

AUTHORS Zhang, W., He, L., Wan, T., Yuan, Z. and Cao, X.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-1999) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Road, Shanghai 200433, P.R. China

FEATURES  
SOURCE Location/Qualifiers  
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BASE COUNT     199 a       376 c       281 g       220 t                  2 others  
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Query Match                   97.0%   Score 1015.4 : DB 9 : Length 1078;  
Best Local Similarity   99.4% : Pred. No. 2.ee-200;  
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Dd	61	cttcctgtttctgaacttgctgcacacatgatcctgtgcccacacatgacctccctccataagggg	120
Oy	128	cacccccaagtcaaggtgacccccacaacgctgaactgctgtgaaacttgcctccctggcag	187
Dd	121	caccccccaagtcacaggtgacccccacaacgctgaactgctgtgaaacttgcctccctggcag	180
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Oy	248	gtgtccaagccttgaggaagcacagcacagaggggagagacagaaggccctcagctaagacc	307
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REFERENCE  
2 (bases 1 to 156899)  
AUTHORS  
Kreemidloots, G., Gardner, A. E., Callen, D. F. and Sutherland, G. R.  
TITLE  
Direct Substitution  
JOURNAL  
Submitted (30-NOV-2001) Cytogenetics & Molecular Genetics, Women's

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 AC022554  
 VERSION AC022554.2 GI:7637249  
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 SOURCE human.  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 157090)  
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 Homo sapiens chromosome, clone RP11-21B21  
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 Zimmer, A., and Zody, M.  
 Direct Submission  
 Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Apr 22, 2000 this sequence version replaced gi:6910631.  
 All repeats were identified using RepeatMasker:  
 Smith, A. F. A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WITB  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L245  
 Center clone name: 21\_B.21  
 ----- Summary Statistics  
 Sequencing vector: M13; M7815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 138238 bases at least Q40  
 Consensus quality: 147017 bases at least Q30

Consensus quality: 150850 bases at least Q20  
 Insert size: 170000; agarose-fp  
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 Quality coverage: 3.5 in Q20 bases; sum-of-contigs  
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 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 35 contigs. The true order of the pieces  
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 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
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 \* 1662 1761: gap of 100 bp  
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 \* 87951 93903: contig of 5953 bp in length  
 \* 93904 94003: gap of 100 bp  
 \* 94004 101488: contig of 7485 bp in length  
 \* 101489 101588: gap of 100 bp  
 \* 101589 109837: contig of 8249 bp in length

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* 109838 109937: gap of 100 bp
* 109938 116942: contig of 7005 bp in length
* 116943 117042: gap of 100 bp
* 117043 124191: contig of 7149 bp in length
* 124192 124291: gap of 100 bp
* 124292 133924: contig of 9633 bp in length
* 133925 134024: gap of 100 bp
* 134025 144057: contig of 10033 bp in length
* 144058 144157: gap of 100 bp
* 144158 157090: contig of 12933 bp in length.

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## FEATURES

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4875. 7439
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7540. 8885
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8986. 11624
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11725. 14597
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19756. 21926
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vector_side:left"
30370. 33304
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misc_feature

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/note="assembly\_fragment"

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Query Match 62.2%; Score 651; DB 2; Length 157090;
Best Local Similarity 97.7%; Pred. No. 5,8e-125;
Matches 671; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

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QY 361 ctccatcaccctcctggaataaccgctgtgacacagatgagacccgctatccacagaagt 420
DB 125129 CTCACCTGTGACACCCGCTCCCGAGTGTGGACACAGGATGAGACCCGTATTCACACAGCT 125188
QY 421 ggccttcgcgagctgcctgtcagagctgtatcatgacagagcgccgcgagacagc 480
DB 125189 GGCCTTCCCGCGAGCTCCTGTGCAGAGCGTGTATCATATGACACGAGCGCCGCGAACAACG 125248
QY 481 tgcgtcaacctcctgcgagctgtctccagagctgtgtgtgcgcgcgcgcgcctgcctc 540
DB 125249 TCGGCTCAACTCTCGTGGGCTCTCCAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 125308
QY 541 ccgcgacgctcgcgggctcccccacaccttgggaccttgccttcacacagatccaca 600
DB 125309 CCGGACGCGCTCGGGGCTCCCGACACCTGGGGCTTGTGCTTCACACGAGTTTCATCA 125368
QY 601 cgtcccgctcggctgcacctgcgtgcgtcccgcttcagtgacgcgagcggtggg 660
DB 125369 CGTCCCGCTCGGCTGCACCTGCGTGTGCGCCGTTTCAGTGTACCGCGCGCGTGGGG 125428
QY 661 cccctaaagctgacacagctgtgtctccacagagcgccctattatgtattatgt 720
DB 125429 CCCCTAAGCTGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 125488
QY 721 tattatattgctcccccacacactacccttgggtgtcgtgcattcccgctgtcagaga 780
DB 125489 TATTTATATAGCTCCCGACACACTACCTTGGGGCTGTGGGCACTTCCCGTGTGTGAGAGA 125548
QY 781 cagcccccacactgtcttcctccatctccagcctcagtagtggggtaagaagagctcagc 840
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QY 841 acctcttcagcccttaagctgcagaaaggtgcacacgagctgcgttactctggctc 900
DB 125609 ACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGCACAGGCTGCTGTACTTGGCTC 125668
QY 901 cctgtcctgcctcgcgcttccttaacctacacagctgcctcagc-cccgcagagctgcct 959
DB 125669 CCTGTCTCTGCTCCCGCTTCCCTTACCTATACATGCTCAGGCCCCGCGAGCTGCT 125728
QY 960 ctccccaacctcctctggaagtaaccctgttcttcaacaattattaaagtgatglat 1019
DB 125729 CTTCACCAACCTCTTGAAGTACCCCTGTCTTAAACATTTATTAAGTGTACGTGTAT 125788
QY 1020 tattaaactgataacacatcccacaa 1046
DB 125789 TATTAACGTAGTAACACATCCCGAGA 125815

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## RESULT 7

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LOCUS Mouse DNA sequence from clone RP23-354124 on chromosome 13,
DEFINITION complete sequence.
ACCESSION AL591003
VERSION AL591003.16 GI:16605732
KEYWORDS HTG.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 221647)
AUTHORS Kay,M.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hunquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk

```



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Db	17490	RACSKRTGSGYSTGSGSMKKKKGYSKSRGMMGKKKTCYCMKKYKRYKRTSMCMWYMYKMSW	17431	
Qy	365	atctcaccccttgagataccgtgtgtgagacacgatatgagacgcgtatccacagaagctgccc	424	
Db	17430	GYSKRRKRCCKMMKKGCTGTGRGMSKKSGYSKSRGMMGSSYSTSCWMSCKGYSMMKCMKMYMS	17371	
Qy	425	cttcgcgcagatgcctctgtgaaagcgctgatatgatgacgaagcgccgcgagagaacgctgcg	484	
Db	17370	YKKKRRSRKGSMSKSGMNGVYAGRCYSSSMSTRKRRKCTYSYSYKKGKRGKMGWGGMK	17311	
Qy	485	ctcacactccgctgcgagctgtccacagagccctgtgtgtgcgcgcgcgcgcgcctgtcccgcc	544	
Db	17310	RGSKWYSMMKMKMRKSRMSWKCTSKSYKSGRRKRSKMGWGSTSKAKSSMRMAGSKCTYSSS	17251	
Qy	545	gacgcgctcgaggctcccccacacacttggggccttgccttcacacacagatcattcacagtc	604	
Db	17250	YMSNNRRNNRNGKCTGCNMYRRSRAMNGNMAAAGCTTCCCAANTNGGGGGAATAAAGGCGC	17191	
Qy	605	ccccgcgcctcacactgtgtgtgtgcgcccgctcagtgatgtgtacgcgcgagccgcttgggcccc	664	
Db	17190	GSASASCTYKGRMSKSCYRSGTRRCKM-----SKCRRSRSGKSMGM	17148	
Qy	665	taagactgcacacgltgtgtcccccagagaggaaccccctattatgtattatgtattt	724	
Db	17147	TRGRSGKTSYSAKSGSGGCTCYCMOWMGKRGKCMSS-RKMMYKYSYRRKRRMTLCKMKCY	17089	
Qy	725	tatatgcctcccccaacacatacctcttgggtgtcttgggaattccccgtgtcttggagaagc	784	
Db	17088	SMYAMMYRSMCMCMCMCKSCCGCYSMGMSYSYSGKYSMGMKSYMRRSRYSKRSRYSKAMR	17029	
Qy	785	ccccacgcgttctctcattccacgcccaagtgtgtgtgggttagaaggaagtcacgacct	844	
Db	17028	SSKRRMGTTGRRKGGGSRYSKGGGSYKGGGSGNGGGRGKSTKSSSGKKSSTYKMSCCARY	16969	
Qy	845	cttccagcccttaaaagcgcagaaaaggtgtcacacgcgtcgtcttaccttgcctctc	904	
Db	16968	KSMYSKYSRMMCMMSYTYCMGCKCMSSCMWMSMRKRSKSGSMAGKMWMDKGSYSTKS	16909	
Qy	905	tcctgtctccgcgcttcccttaccctatactgagcgtcctcagcccgacgctgctctcc	964	
Db	16908	DKMBRSBSKYSKMSMSRGRKYCTDMSKMYTTCGAGANGCCGTACCTAGCTGGTTC	16849	
Qy	965	caactcctcttggaaatc	982	
Db	16848	CCACAGGGGGGTAAAGTTC	16831	
RESULT	9			
LOCUS	AF429315	125020 bp	DNA	linear PRI 18-JAN-2002
DEFINITION	Homo sapiens junctophillin 3 (JPH3) gene, partial cds.			
ACCESSION	AF429315			
VERSION	AF429315.1	GI:17646244		
KEYWORDS	human.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 125020)			
AUTHORS	Holmes,S.E., O'Hearn,E., Rosenblatt,A., Callahan,C., Hwang,H.S., Ingersoll-Asmworth,R.G., Fleisher,A., Stevanin,G., Brice,A., Potter,N.T., Ross,C.A. and Margolis,R.L.			
TITLE	A repeat expansion in the gene encoding junctophillin-3 is associated with Huntington disease-like 2			
JOURNAL	Nat. Genet. 29 (4), 377-378 (2001)			
MEDLINE	21583737			
PUBMED	11694876			
REFERENCE	2 (bases 1 to 125020)			

AUTHORS	Holmes,S.E., Inderroll,Ashworth,R.G., Ross,C.A. and Margolis,R.L.
TITLE	Direct Submission
JOURNAL	Submitted (05-Oct-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
FEATURES	Location/Qualifiers
source	1..125020 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="16" /map="16q24.3; between D16S520 and WI-12410" /note="Isolated from a patient with Huntington's disease-like 2 (HDL2)" complement(35581..35746) /rpt_type=cadem /rpt_unit=ctg complement(<36507..>36887) /gene="JPH3" /product="junctionhilin 3" complement(<36507..>36887) /gene="JPH3" /note="Jp3" complement(<36507..36887) /gene="JPH3" /note="component of the junctional complex between plasma membrane and endoplasmic reticulum" /codon_start=1 /product="junctionhilin 3" /protein_id="AAI40941.1" /db_xref="GI:1646245" /translation="MSSGGRNFDDGSYCGGWEDKAHGVCYTPGGQGEYTSMS HGFEVLCYTWPNSNTYQGTWAGTAKRHIGLGIESKGVYKGEWHGKRGYREGCG NGAEVETWSNGLDGTEITSDG"
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mRNA	
repeat_region	
BASE COUNT	29056 a 32731 c 30696 g 28283 t 4254 others
ORIGIN	
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Best Local Similarity	11.7%; Fred. No. 0.0085;
Matches	88; Conservatvie 315; Mismatches 344; Indels 5; Gaps 1;
Dy	27 cagcgtcccccgcctccgccaccatgaacgtctctcccgacctgttctgacctgac 86
Db	17136 SRSAMCCSTCYACCKSMCTSCYIGMSMKGYIACSYRGSMSKYCMRSTYSTSGCCT 17195
Oy	87 tgacaacatgctgcggcccaatgacccctcccttaaggaggagccccacagtacagta 146
Db	17196 TTTTCGCCCNATMTGGGAAGCTTTTNCKNKITYTRKRRCGAMCKYNNYNINSMSSGRA 17255
Oy	147 cccacactgctactcgtcgttagaagactgccccttcgcagcagccccccacactgtcg 206
Db	17256 GMSCTKYRKSSMTMASVCMWKS-----MYCSMRSMASRGMWSGSYMMKMSSWRMSCY 17310
Oy	207 ctccgagtgccaaatggggggcagcgtttgacctgacctggtgtgccagctcgagagcg 266
Db	17311 MCCCMCMKKCYCMMSMRBRGMSYTYVASWSSSGCYCTRWCWSSSKCYKSTYMMMR 17370
Oy	267 caagcacagggggagggcagcagaagccctacagctaacacagctgcgcgtgctgcgcg 326
Db	17371 SKRMKGMSKRWGSMWMSASRSSCYKCYKSRMGMSKCYRCAAGCMAMGMYRYMYRC 17430
Oy	327 cggaggaagtglttgagagcagacaccacacacagcgtcatcattacacctggaatacg 386
Db	17431 WSMKRRMWKSAmyRMRMRWKRGAMMCMKCYSRMSRCHMMKMSYCASCRCAMSGTY 17490
Oy	387 tggacacagatgagacgcgtatccaagaagctgaccttcgacgagcgtgctgcaag 446
Db	17491 MGCASIMCMSYTCWTCTSYSTRYRCTWCWCGWSSYTKSSKWSSSMSTYKGRKSTYM 17550
Oy	447 gctgtatcagatcacaggaagcgccgagacagctgcctaacacccgtgcgcgtgcc 506
Db	17551 CCTSGAMSCMRCCYMKRASASSMRAGSMSRRRAKRSNMGGRKMMTMGMMRSMKYTYCT 17610
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[illegible]

	Query Match	5.4%	Score 56.8	DB 6,	Length 1754;	
	Best Local Similarity	51.2%;	Pred. No. 0.077;			
	Matches 133;	Conservative 0;	Mismatches 127;	Indels 0;	Gaps 0;	
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Db	255 CACCACACTGTGGCGAACGCTGTGCCTCTGGGCCATCAGAAATTCCTCATCGACCCGCGAGGTA	314				
QY	409 tccacaagaagctggcgcttcgcgcgaagtgtcgtttgacagaagcttatcgattgacagaagcg	468				
Db	315 CCCCAAGTACTGCTTGANAGCTAATGCTGTGTGCCGGGGCTCTGACCCGGGCTTTCCG	374				
QY	469 ccgcgagacagctgcgtccaactccgtltygcgctgtcttcagaagaactgtgtgtltygcgcg	528				
Db	375 CGAGAGGAGACGTGCGCTTCCGAGGCCCCCTGTCTACATGCCACCGTGTCTCTGCGCG	434				
QY	529 ccgcgcgcgcgtccgcgcgcgaagctcggaggctcccacaaacttgggccttgccttacac	588				
Db	435 CACCCCGCTGTCGGCGGCGCGCTTCCGTCTACACGAGGGCTTAGTACCATCCCGT	494				
QY	589 cgagttatatccaagtccccg	608				
Db	495 GGGCTGCACCTGGCTCCCG	514				

RESULT	12
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LOCUS	AF458059 486 bp mRNA linear PRI 15-JAN-2002
DEFINITION	Homo sapiens IL25 mRNA, complete cds.
ACCESSION	AF458059
VERSION	AF458059.1 GI:18034675
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 486)
AUTHORS	Fort,M.M., Cheung,J., Yen,D., Li,J., Zurawski,S.M., Lo,S., Menon,S., Clifford,T., Hunte,B., Lesley,R., Muchamuel,T., Hirst,S.D., Zurawski,G., Leach,M.W., Gorman,D.M. and Rennick,D.M.
TITLE	IL-25 induces IL-4, IL-5, and IL-13 and Th2-associated Pathologies
JOURNAL	In Vivo
MEDLINE	Immunity 15 (6), 985-995 (2001) 21629216



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QY 401 gaccgtatccacagagagcgtgcttcgcccagtgccctgacagagcgtatgata 460  
DB 405 AACCGGCTCCCGAGAGCGTGTACACAGCCGCTGTGCTGTGCGGCACTGCGTACCA 464  
QY 461 cggagcgcccgagacagcgtgct---caactcgtgagcgtgctccagagcgtgctg 517  
DB 465 CAACAGAGGCTCCACATGAGACCCCGGAGCACTCGAGCTGCTTACACACAGCACT 524  
QY 518 gtgtctgagcgccgagcgtgctcccgaga 546  
DB 525 GTCTTACCGCGCGCCATGCGCA 553

## RESULT 15

AY034088 462 bp mRNA linear ROD 03-DEC-2001

LOCUS AY034088 Mus musculus Interleukin 17E precursor, mRNA, partial cds.

DEFINITION AY034088

ACCESSION AY034088.1 GI:17266279

VERSION

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 462)

AUTHORS Pan, G., French, D., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J., Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P., and Gurney, A. L.

TITLE Direct Submission

JOURNAL Submitted (08-MAY-2001) Molecular Biology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA

MEDLINE J. Immunol. 167 (11), 6559-6567 (2001)

PUBMED 11714825

REFERENCE 2 (bases 1 to 462)

AUTHORS Pan, G., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J., Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P., and Gurney, A. L.

TITLE Direct Submission

JOURNAL Submitted (08-MAY-2001) Molecular Biology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA

MEDLINE J. Immunol. 167 (11), 6559-6567 (2001)

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REFERENCE 2 (bases 1 to 462)

AUTHORS Pan, G., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J., Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P., and Gurney, A. L.

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MEDLINE J. Immunol. 167 (11), 6559-6567 (2001)

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REFERENCE 2 (bases 1 to 462)

AUTHORS Pan, G., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J., Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P., and Gurney, A. L.

TITLE Direct Submission

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REFERENCE 2 (bases 1 to 462)

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TITLE Direct Submission

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MEDLINE J. Immunol. 167 (11), 6559-6567 (2001)

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TITLE Direct Submission

JOURNAL Submitted (08-MAY-2001) Molecular Biology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA

MEDLINE J. Immunol. 167 (11), 6559-6567 (2001)

PUBMED 11714825

REFERENCE 2 (bases 1 to 462)

AUTHORS Pan, G., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J., Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P., and Gurney, A. L.

TITLE Direct Submission

JOURNAL Submitted (08-MAY-2001) Molecular Biology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA

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REFERENCE 2 (bases 1 to 462)

AUTHORS Pan, G., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J., Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P., and Gurney, A. L.

TITLE Direct Submission

JOURNAL Submitted (08-MAY-2001) Molecular Biology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA

MEDLINE J. Immunol. 167 (11), 6559-6567 (2001)

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REFERENCE 2 (bases 1 to 462)

AUTHORS Pan, G., Mao, W., Maruoka, M., French, D., Risser, P., Lee, J., Foster, J., Aggarwal, S., Nicholes, K., Guillet, S., Schow, P., and Gurney, A. L.

TITLE Direct Submission

JOURNAL Submitted (08-MAY-2001) Molecular Biology, Genentech, 1 DNA Way, South San Francisco, CA 94080, USA

MEDLINE J. Immunol. 167 (11), 6559-6567 (2001)

QY 400 gaccgtatccacagagcgtgcttcgcccagtgccctgacagagcgtatgatac 459  
DB 222 GATGAGACCCCTCAACAGCAGGCGGCATCTCCCTGGAGATAGTGGACAGACGCTTG 281  
QY 460 acgagcgagcgccgagacagcgtgct---caactcgtgagcgtgctccagagcgtgctg 516  
DB 282 ACAGAGAGGCTCCACATGAGACCCCGTGGCAACTCCGTCACATTTACACACACAGC 341  
QY 517 gtgtctgagcgccgagcgtgctcccgaga 548  
DB 342 GTCTTACCGCGCGCCATGCGCA 553

Search completed: September 4, 2002, 01:49:32  
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 00:42:23 : Search time 202.95 seconds  
(without alignments)  
8857.400 Million cell updates/sec

Title: US-09-854-280-4  
Perfect score: 1047  
Sequence: 1 gccagcgtgcagcgcgtc.....tgatgaacacatcccaaaa 1047

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : N.Geneseq.032802:\*

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22:	/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT.*
23:	/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.*
24:	/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1047	100.0	21	AAA96338	CDNA encoding a no
2	1047	100.0	21	AA229728	Human Interleukin
3	1047	100.0	22	AA546148	Human DNA encoding
4	1047	100.0	22	AA509510	Human CDNA encoding
5	1028.4	98.2	21	AAA58991	CDNA encoding a hu
6	1028.4	98.2	21	AAA59149	CDNA encoding a hu
7	1006.4	96.1	21	AA236836	Nucleotide sequenc
8	1006.4	96.1	23	AA167878	Human Interleukin
9	923.4	88.2	22	AA15291	Human Interleukin

10	640.4	61.2	705	21	AA236834	Partial nucleotide
11	640.4	61.2	705	23	AA167876	Human Interleukin
12	591	56.4	591	21	AAA09153	Human Interleukin
13	274.8	26.2	521	21	AAA58990	CDNA encoding a hu
14	273.8	26.2	521	21	AAA58989	CDNA encoding a hu
15	273.8	26.2	521	21	AAA59147	CDNA encoding a hu
16	273.8	26.2	521	21	AAA59148	CDNA encoding a hu
17	230	22.0	230	21	AA229731	Virtual DNA Itagme
18	143.8	13.7	332	21	AA236856	CDNA clone HTGCD19
19	56.8	5.4	454	21	AAA58982	CDNA encoding a hu
20	56.8	5.4	454	21	AAA59156	CDNA encoding a ra
21	56.8	5.4	522	21	AA236837	Partial nucleotide
22	56.8	5.4	522	23	AA167888	Human Interleukin
23	56.8	5.4	1385	21	AAA58983	CDNA encoding a hu
24	56.8	5.4	1385	21	AAA59155	CDNA encoding a hu
25	56.8	5.4	1642	23	AA236835	Partial nucleotide
26	56.8	5.4	1642	23	AA167877	Human Interleukin
27	56.8	5.4	1794	22	AA509512	Human CDNA encodin
28	56.8	5.4	1819	21	AA252195	Human transforming
29	56.8	5.4	2361	21	AA252201	Human transforming
30	53.8	5.1	504	21	AAA58986	CDNA encoding a hu
31	53.8	5.1	504	21	AAA59158	CDNA encoding a hu
32	53.8	5.1	504	24	ABA02393	Human Interleukin
33	53.8	5.1	644	24	ABA03213	Human IL-17 recept
34	53.6	5.1	985	21	AAA58988	CDNA encoding a mu
35	53.6	5.1	985	21	AAA59160	CDNA encoding a mu
36	53.6	5.1	985	24	ABA02394	Murine Interleukin
37	52.2	5.0	1320	22	AA509511	Human CDNA encodin
38	52.2	5.0	1320	22	AA589569	Native sequence of
39	52.2	5.0	1320	22	AA589569	Human PRO10272 CDN
40	49.8	4.8	1127	21	AAA02477	Human colon cancer
41	49.4	4.7	620	21	AAA58987	CDNA encoding a mu
42	49.4	4.7	2561	22	AA26500	CDNA encoding a mu
43	47.4	4.5	114955	20	AA53491	Rabbit low density
44	47.2	4.5	1032	19	AAV50486	Human adenosine Al
45	46.8	4.5	1032	19	AAV50486	Streptomyces Clavu

## ALIGNMENTS

RESULT	1
ID	AAA96338
AAA96338	standard; cDNA; 1047 BP.
AC	AAA96338:
XX	
DT	08-FEB-2001 (first entry)
XX	
DE	cdna encoding a novel polypeptide designated PRO1122.
XX	
KW	Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;
KW	PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
KW	PRO4352; PRO4380; PRO4354; PRO5737; PRO4425; PRO6030;
KW	PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;
KW	Insulinemia; kidney disorder; Bergers disease; nephropathy;
KW	Schönlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW	Crohn's disease; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	CD5
FT	sig_peptide
FT	Location/Qualifiers
FT	50..643
FT	/*tag= a
FT	/*tag= b
PD	MO200056889-A2.
XX	28-SEP-2000.
XX	01-MAR-2000; 2000WO-US05601.

PR 23-MAR-1999; 9905-0125774.  
 PR 23-MAR-1999; 9905-0125778.  
 PR 24-MAR-1999; 9905-0125826.  
 PR 31-MAR-1999; 9905-0127035.  
 PR 05-APR-1999; 9905-0127706.  
 PR 21-APR-1999; 9905-0130359.  
 PR 27-APR-1999; 9905-0131270.  
 PR 27-APR-1999; 9905-0131272.  
 PR 04-MAY-1999; 9905-0132371.  
 PR 04-MAY-1999; 9905-0132379.  
 PR 04-MAY-1999; 9905-0132383.  
 PR 25-MAY-1999; 9905-0135750.  
 PR 08-JUN-1999; 9905-0138166.  
 PR 20-JUL-1999; 9905-0144791.  
 PR 03-AUG-1999; 9905-0146970.  
 PR 09-DEC-1999; 9905-0170262.  
 XX (GETH ) GENENTECH INC.  
 PA Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;  
 PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;  
 XX P-PSDB; AAB18911.  
 DR WPI; 2000-628263/60.  
 XX  
 XX Novel secreted and transmembrane polypeptides useful for diagnosing  
 PT tumour in a mammal, for identifying agonists and antagonists of the  
 PT polypeptide and for therapeutic use  
 PS Claim 2; Fig 5; 222pp; English.  
 XX  
 CC The present sequence encodes a secreted or transmembrane polypeptide.  
 CC The specification describes polypeptides designated PRO1484, PRO4334,  
 CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4405,  
 CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO4425, PRO5990,  
 CC PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is  
 CC useful for diagnosing tumour in a mammal. The polypeptides, their  
 CC agonists and antagonists are useful treating a condition associated with  
 CC expression or activity of the polypeptide. Conditions treated include  
 CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are  
 CC capable of inducing proliferation of mammalian kidney mesangial cells  
 CC and are therefore useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger's disease or other  
 CC nephropathies associated with Schönlein-Henoch purpura, celiac disease,  
 CC dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used  
 CC to generate transgenic animals for use in development and screening of  
 CC therapeutically useful reagents and also for chromosome identification  
 CC and tissue typing.  
 CC  
 XX Sequence 1047 BP; 177 A; 381 C; 280 G; 209 T; 0 other;

Query Match 100.0%; Score 1047; DB 21; Length 1047;  
 Best Local Similarity 100.0%; Pred. No. 8, 6e-241;  
 Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccaaggtgtaagagcgctccaagccagctgcgcgcgttcgacacatgaagctccct 60  
 DB 1 gccaaggtgtaagagcgctccaagccagctgcgcgcgttcgacacatgaagctccct 60  
 QY 61 ccccgagctcctgtttctgacactggtcgtcacacatgcttggccacatgaagctccct 120  
 DB 61 ccccgagctcctgtttctgacactggtcgtcacacatgcttggccacatgaagctccct 120  
 QY 121 cagggggacaccccaagtaaggtacccaactgctactcgggtgtaagaaagctccct 180  
 DB 121 cagggggacaccccaagtaaggtacccaactgctactcgggtgtaagaaagctccct 180  
 QY 181 cggcgaagccccccacacactgctggtcgaaggtgacaaagtgagggggaaggttgcctgt 240  
 DB 181 cggcgaagccccccacacactgctggtcgaaggtgacaaagtgagggggaaggttgcctgt 240

QY 241 agccctggtgtccaagctcgtgaggaagcaagccacaaagggggaagcaagagccctcagc 300  
 DB 241 agccctggtgtccaagctcgtgaggaagcaagccacaaagggggaagcaagagccctcagc 300  
 QY 301 taagaccacgtgcccgtgtgttgcggcgaggaggtgtttgaggacacaccccacagc 360  
 DB 301 taagaccacgtgcccgtgtgttgcggcgaggaggtgtttgaggacacaccccacagc 360  
 QY 361 ctccatccacccctggagataccgtgttgagacagaaagaaagacccgcatcacagaagct 420  
 DB 361 ctccatccacccctggagataccgtgttgagacagaaagaaagacccgcatcacagaagct 420  
 QY 421 ggccttcgcagagtgctcgtgtgacagagcgtatcatgatacagcagggccgcagacagc 480  
 DB 421 ggccttcgcagagtgctcgtgtgacagagcgtatcatgatacagcagggccgcagacagc 480  
 QY 481 tgcgttaactcgtgtgaggtgtgtcccaagacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540  
 DB 481 tgcgttaactcgtgtgaggtgtgtcccaagacgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540  
 QY 541 ccgcgaagctcggggtggtcccccacacactggggccttgccttcacacagagttaccca 600  
 DB 541 ccgcgaagctcggggtggtcccccacacactggggccttgccttcacacagagttaccca 600  
 QY 601 cgtcccgctgagctgacactgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660  
 DB 601 cgtcccgctgagctgacactgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 660  
 QY 661 cccctaaactggagagtggtgtgtgtcccaaggggagacccctattatgtattatgt 720  
 DB 661 cccctaaactggagagtggtgtgtgtcccaaggggagacccctattatgtattatgt 720  
 QY 721 tattatattgcttcccccaacactacccttggggtgtgtgtgtgtgtgtgtgtgtgtgtgt 780  
 DB 721 tattatattgcttcccccaacactacccttggggtgtgtgtgtgtgtgtgtgtgtgtgt 780  
 QY 781 cagcgcacacactgtttccctcatctcagactcagactgagtggtgtgtgtgtgtgtgtgt 840  
 DB 781 cagcgcacacactgtttccctcatctcagactcagactgagtggtgtgtgtgtgtgtgtgt 840  
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 DB 841 acccttcacagccttaagactgagaaaggtgtcacacagcgtgtgtgtgtgtgtgtgtgt 900  
 QY 901 ccttctgtgtcccggtgttccctaccatcactgagcctcagcctcagcagcgtgtgtgt 960  
 DB 901 ccttctgtgtcccggtgttccctaccatcactgagcctcagcctcagcagcgtgtgtgt 960  
 QY 961 ttcccaactccttggagaagtaacccctgtttcttaaacatatttaagtgtaagtgat 1020  
 DB 961 ttcccaactccttggagaagtaacccctgtttcttaaacatatttaagtgtaagtgat 1020  
 QY 1021 attaaactgtatgaacatcccccaaa 1047  
 DB 1021 attaaactgtatgaacatcccccaaa 1047  
 RESULT 2  
 ID AA229728 standard; cDNA; 1047 BP.  
 XX AA229728;  
 XX 27-MAR-2000 (first entry)  
 DE Human Interleukin 17C, PRO1122 cDNA.  
 KW Interleukin; IL-17C; PRO1122 polypeptide; clone DMA62377-1381-1; UNQ561;  
 KW cytokine IL-17; cytotoxic T-lymphocyte-associated antigen 8; CTLA-8;  
 KW hybridisation probe; antigen; antagonist; degenerative cartilaginous disorder;  
 KW agonist; diagnosis; therapy; ss.  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH sig\_peptide 50..103  
 FT /tag- a  
 FT mat\_peptide 50..634  
 FT /tag- b  
 FT /label- Mature\_Interleukin\_17C\_polypeptide  
 FT /note- "Designated as clone DNA62377-1381-1"  
 XX  
 XX MO9960127-A2.  
 XX  
 XX  
 XX PD 25-NOV-1999.  
 XX  
 XX PF 14-MAY-1999; 99MO-US10733.  
 XX  
 XX PR 15-MAY-1998; 98US-0085579.  
 XX PR 23-DEC-1998; 98US-0113621.  
 XX  
 XX PA (GETH ) GENENTECH INC.  
 XX  
 XX PI Chen J, Filvaroff E, Goddard A, Gurney AL, Li H, Wood WT;  
 XX  
 XX DR WPI: 2000-116314/10.  
 XX DR P-PSDB: AAY44460.  
 XX  
 XX PT New polypeptides designated PRO1031 and PRO1122 used to treat a  
 XX PT degenerative cartilaginous disorder  
 XX PS Claim 2: Fig 4; 141p; English.  
 XX  
 XX The present sequence is the cDNA clone DNA62377-1381-1, encoding the  
 CC human PRO1122 polypeptide, also referred to as UNQ561, and as  
 CC interleukin-17C (IL-17C). This sequence has identity with the  
 CC cytokine IL-17 and cytotoxic T-lymphocyte-associated antigen 8 (CTLA-8).  
 CC PRO1122 is expressed in pancreas, small intestine, stomach and testis  
 CC also. It shares about 26-28% amino acid identity with IL-17 and IL-17B.  
 CC The entire coding region of IL-17C can be used as hybridisation probe.  
 CC The PRO1122 polypeptide, agonist or antagonist, is used to diagnose and  
 CC treat a degenerative cartilaginous disorder.  
 XX  
 XX Sequence 1047 BP; 177 A; 381 C; 280 G; 209 T; 0 other;  
 SQ

Query Match 100.0%; Score 1047; DB 21; Length 1047;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-241;  
 Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccagggtgcaagcgctcccaagccagcctgcccgcgtgcccgcacacatgacgtcct 60  
 |||||  
 DB 1 gccagggtgcaagcgctcccaagccagcctgcccgcgtgcccgcacacatgacgtcct 60  
 |||||  
 QY 61 ccccgccctcctgttctgaactgctgcaacatgctgccccacatgacccctcct 120  
 |||||  
 DB 61 ccccgccctcctgttctgaactgctgcaacatgctgccccacatgacccctcct 120  
 |||||  
 QY 121 cagggggacccccacagtcacgttacccccacactgactgctgaggaactgcct 180  
 |||||  
 DB 121 cagggggacccccacagtcacgttacccccacactgactgctgaggaactgcct 180  
 |||||  
 QY 181 cggcagagccccccacacactgctgctcagagtgccaaagtggggcagcttgcctgt 240  
 |||||  
 DB 181 cggcagagccccccacacactgctgctcagagtgccaaagtggggcagcttgcctgt 240  
 |||||  
 QY 241 agccctggtgtcagcctgagcagcaagccacaggggagagcagagagccctcagc 300  
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 DB 241 agccctggtgtcagcctgagcagcaagccacaggggagagcagagagccctcagc 300  
 |||||  
 QY 301 tacgacccagtgcccggtgctgcgcgcgagagagtgcttgagagcagacccccacagc 360  
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 DB 301 tacgacccagtgcccggtgctgcgcgcgagagagtgcttgagagcagacccccacagc 360  
 |||||  
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 |||||

DB 361 ctccatctcaccttgagagatccgtgtgacacagatgagagcgtatccacagaagct 420  
 |||||  
 QY 421 gcccttcgcagagtgctcgtgacagagcgtgtatcatgacagcagggcgccgacagc 480  
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 DB 421 gcccttcgcagagtgctcgtgacagagcgtgtatcatgacagcagggcgccgacagc 480  
 |||||  
 QY 481 tgcgtcacaactcgtgagcgtgtccacagacgtgtgctgctgcgcgcgcgcctgtc 540  
 |||||  
 DB 481 tgcgtcacaactcgtgagcgtgtccacagacgtgtgctgctgcgcgcgcgcctgtc 540  
 |||||  
 QY 541 ccgcagcagcgtcggggctcccccacacactgaggccttgccttccacacagagttatcca 600  
 |||||  
 DB 541 ccgcagcagcgtcggggctcccccacacactgaggccttgccttccacacagagttatcca 600  
 |||||  
 QY 601 cgtcccgctgcgtgacactgctgtgtgcccgttcagtgatcagcgcagagcgtggg 660  
 |||||  
 DB 601 cgtcccgctgcgtgacactgctgtgtgcccgttcagtgatcagcgcagagcgtggg 660  
 |||||  
 QY 661 cccctagactgacacgtgtgctcccccagagggaccccctattatgtattatgt 720  
 |||||  
 DB 661 cccctagactgacacgtgtgctcccccagagggaccccctattatgtattatgt 720  
 |||||  
 QY 721 tattatatagtcctcccccacacactacccttgggtctgggcatcccgctgtcggaga 780  
 |||||  
 DB 721 tattatatagtcctcccccacacactacccttgggtctgggcatcccgctgtcggaga 780  
 |||||  
 QY 781 cagccccccacgtgtcctcctatctccagcctcagtagtggggagagaagagctcagc 840  
 |||||  
 DB 781 cagccccccacgtgtcctcctatctccagcctcagtagtggggagagaagagctcagc 840  
 |||||  
 QY 841 acctcttcacgccttaaaagctgacagaaagtgctacacagcgtgctgtacttggctc 900  
 |||||  
 DB 841 acctcttcacgccttaaaagctgacagaaagtgctacacagcgtgctgtacttggctc 900  
 |||||  
 QY 901 cctgtctcgtcccggtctcccttaccatactgactcagcagcccgacagctgctc 960  
 |||||  
 DB 901 cctgtctcgtcccggtctcccttaccatactgactcagcagcccgacagctgctc 960  
 |||||  
 QY 961 ttcccaactccttggagtaaccctgttcttaacaattatgaagtgactgtatt 1020  
 |||||  
 DB 961 ttcccaactccttggagtaaccctgttcttaacaattatgaagtgactgtatt 1020  
 |||||  
 QY 1021 attaaactgatgaacacatccccaana 1047  
 |||||  
 DB 1021 attaaactgatgaacacatccccaana 1047  
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RESULT 3  
 ID AAS46148 standard; cDNA; 1047 BP.  
 AC AAS46148;  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human DNA encoding PRO polypeptide sequence #224.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200168848-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001MO-US06520.  
 XX  
 PR 01-MAR-2000; 2000MO-US05601.  
 PR 02-MAR-2000; 2000MO-US05841.

PR 03-MAR-2000; 2000US-187202P.  
 PR 06-MAR-2000; 2000US-186968P.  
 PR 14-MAR-2000; 2000US-189320P.  
 PR 14-MAR-2000; 2000US-189328P.  
 PR 15-MAR-2000; 2000MO-US06884.  
 PR 21-MAR-2000; 2000US-190828P.  
 PR 21-MAR-2000; 2000US-191007P.  
 PR 21-MAR-2000; 2000US-191048P.  
 PR 21-MAR-2000; 2000US-191314P.  
 PR 28-MAR-2000; 2000US-192655P.  
 PR 29-MAR-2000; 2000US-193032P.  
 PR 29-MAR-2000; 2000US-193053P.  
 PR 30-MAR-2000; 2000MO-US08439.  
 PR 04-APR-2000; 2000US-194449P.  
 PR 04-APR-2000; 2000US-194647P.  
 PR 11-APR-2000; 2000US-195975P.  
 PR 11-APR-2000; 2000US-196000P.  
 PR 11-APR-2000; 2000US-196187P.  
 PR 11-APR-2000; 2000US-196680P.  
 PR 11-APR-2000; 2000US-196820P.  
 PR 18-APR-2000; 2000US-198121P.  
 PR 18-APR-2000; 2000US-198585P.  
 PR 25-APR-2000; 2000US-199397P.  
 PR 25-APR-2000; 2000US-199550P.  
 PR 25-APR-2000; 2000US-199654P.  
 PR 03-MAY-2000; 2000US-201516P.  
 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14841.  
 PR 02-JUN-2000; 2000MO-US15264.  
 PR 05-JUN-2000; 2000US-209832P.  
 PR 28-JUL-2000; 2000MO-US20710.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000MO-US23328.  
 PR 08-NOV-2000; 2000MO-US30952.  
 PR 01-DEC-2000; 2000MO-US32676.  
 PR 20-DEC-2000; 2000MO-US34956.  
 XX  
 PA (GENETH ) GENENTECH INC.  
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI, 2001-602746/68.  
 XX P-PSDB; AA029247.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumours, such as prostate and breast tumours, in mammals and  
 PT to screen for modulators of the compounds -  
 XX  
 PS Claim 2; Fig 447; 774pp; English.

XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
 CC primers for PRO polypeptides of the invention. The sequences of the  
 CC invention can be used to detect the presence of a tumour in a mammal by  
 CC comparing the level of expression of a PRO polypeptide in a test sample  
 CC of cells from the animal and a control sample of normal cells, whereby a  
 CC higher level of expression in the test sample indicates the presence of a  
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
 CC blood, when contacted with it. A specific polypeptide can be used to  
 CC stimulate the proliferation or differentiation of chondrocyte cells. The  
 CC PRO proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders.  
 XX  
 SQ Sequence 1047 BP; 177 A; 381 C; 280 G; 209 T; 0 other;

Query Match

100.0%; Score 1047; DB 22; Length 1047;

Best Local Similarity 100.0%; Pred. No. 8, 6e-241;  
 Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	gccaggtgtcagagccgctccaagccagcctgcccgcgtgcgcgcacatgaagctcct	60
QY	61	ccccgcctcctgtttctgcacctgtgcacacatgctcgtgccacatataccctcct	120
DB	61	ccccgcctcctgtttctgcacctgtgcacacatgctcgtgccacatataccctcct	120
QY	121	cagggggcaccaccacagtcaggttacccacactgtctatctggcttgaagaatgccct	180
DB	121	cagggggcaccaccacagtcaggttacccacactgtctatctggcttgaagaatgccct	180
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DB	181	cgagcagggcccccccaacctgtcgtcaggttgcacagttgggggagagcttgcctgt	240
QY	241	agccctgtgttccagccttgagagcagcaagccacaggggagagcagagagccctcagc	300
DB	241	agccctgtgttccagccttgagagcagcaagccacaggggagagcagagagccctcagc	300
QY	301	tacgaccacagtcgcgggtgtcgcgcggagagaggtgttggagggcagacacaccacagc	360
DB	301	tacgaccacagtcgcgggtgtcgcgcggagagaggtgttggagggcagacacaccacagc	360
QY	361	ctccatctaccccttgagagataacggttgtgagcagagatgaagagccgtatccacaagaagct	420
DB	361	ctccatctaccccttgagagataacggttgtgagcagagatgaagagccgtatccacaagaagct	420
QY	421	ggccttcggcagtgctcgtgtgcagagagctgtatcagatgcacagagcgccgcagacagc	480
DB	421	ggccttcggcagtgctcgtgtgcagagagctgtatcagatgcacagagcgccgcagacagc	480
QY	481	tgcgtcaactcgtgcgggtgtcgtccagagcgtgtgtgtgtgcgcgcgcgcgtgtc	540
DB	481	tgcgtcaactcgtgcgggtgtcgtccagagcgtgtgtgtgtgtgcgcgcgcgcgtgtc	540
QY	541	cgcgagcgtgtgcgggtgtcgtccacacactggggccttgccttcaaacggaattatcca	600
DB	541	cgcgagcgtgtgcgggtgtcgtccacacactggggccttgccttcaaacggaattatcca	600
QY	601	cgctcccgctgcgtgcacgtgtgtcgtcccgcttcaagttgagcgcggagcgctgtgtgt	660
DB	601	cgctcccgctgcgtgcacgtgtgtcgtcccgcttcaagttgagcgcggagcgctgtgtgt	660
QY	661	cccttagactgagacagtggtgtcgtccagagggcacccctattatgtattatgt	720
DB	661	cccttagactgagacagtggtgtcgtccagagggcacccctattatgtattatgt	720
QY	721	tatttatgtcctcccccacactaaccttggtgggtctgggcatcccccgtgttgagga	780
DB	721	tatttatgtcctcccccacactaaccttggtgggtctgggcatcccccgtgttgagga	780
QY	781	cagccccccactgttctcccatctccagcctcagtagttgggggtagaagagccagc	840
DB	781	cagccccccactgttctcccatctccagcctcagtagttgggggtagaagagccagc	840
QY	841	acctcttcaagcccttaagcttgacagaaaggtgtcaacacgctgtcctgtaccttgctc	900
DB	841	acctcttcaagcccttaagcttgacagaaaggtgtcaacacgctgtcctgtaccttgctc	900
QY	901	ccgtgtcgtctccggctcccttaccctatactatctgctcagcccgagagctgtcctc	960
DB	901	ccgtgtcgtctccggctcccttaccctatactatctgctcagcccgagagctgtcctc	960
QY	961	ttcccaacctccttggaaagtaaccctgtttcttaaacatatttaagtgtacgttatt	1020
DB	961	ttcccaacctccttggaaagtaaccctgtttcttaaacatatttaagtgtacgttatt	1020
QY	1021	attnaactgtatgacacatccccaaaa	1047
DB	1021	attnaactgtatgacacatccccaaaa	1047

DB 1021 attaaactgatgacacatcccaaaa 1047

RESULT 4

AA09510

AA09510 standard; cDNA, 1047 BP.

AC AA09510;

DT 24-OCT-2001 (first entry)

XX

DE Human cDNA encoding Interleukin 17C ligand, IL-17C.

XX

KW Human: Interleukin-17C ligand; IL-17C; agonist; antagonist; ss;

KW PRO1122: DNA 62377-1381-1; systemic lupus erythematosus;

KW Rheumatoid arthritis; osteoarthritis; diabetes mellitus;

KW allergic disease; asthma; demyelinating disease;

KW degenerative cartilaginous disorder; transplantation associated disease.

XX

OS Homo sapiens.

XX

FT Key Location/Qualifiers

FT CDS 50..643

FT /\*tag= a

FT /\*product= "IL-17C"

FT sig\_peptide 50..103

FT /\*tag= b

FT mat\_peptide 104..640

FT /\*tag= c

FT /label= Mature\_IL\_17C

XX

PN W0200146420-A2.

XX

PD 28-JUN-2001.

XX

PF 20-DEC-2000; 2000WO-US34956.

XX

PR 23-DEC-1999; 99US-0172096.

PR 30-DEC-1999; 99WO-US31274.

PR 11-JAN-2000; 2000US-0175481.

PR 18-FEB-2000; 2000WO-US04341.

PR 02-MAR-2000; 2000WO-US05841.

PR 21-MAR-2000; 2000US-0191007.

PR 21-MAR-2000; 2000WO-US07532.

PR 02-JUN-2000; 2000WO-US15264.

PR 22-JUN-2000; 2000US-0213087.

PR 22-AUG-2000; 2000US-0644848.

PR 24-AUG-2000; 2000WO-US23328.

PR 24-OCT-2000; 2000US-0242837.

PR 10-NOV-2000; 2000WO-US30873.

PR 28-NOV-2000; 2000US-0253646.

PR 01-DEC-2000; 2000WO-US32678.

XX

PA (GETH ) GENENTECH INC.

XX

PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;

PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL,

PI Watanabe CK, Williams PM, Wood WI, Yansura DG;

XX

DR WPI: 2001-451708/48.

DR P-PSDB: AAU04951.

XX

PT Novel PRO polypeptides homologous to interleukin-17, useful for the

PT diagnosis and treatment of immune related disease e.g. rheumatoid

PT arthritis and diabetes -

XX

PS Claim 1; Fig 3; 188pp; English.

XX

CC The sequence (DNA 62377-1381-1) encodes a PRO polypeptide (PRO1122)

CC which is the human interleukin 17C ligand, IL-17C. A composition

CC containing ant/agonists to the PRO polypeptides or individual components

CC are useful for treating a mammal with an immune related disease, e.g.

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,

CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an

CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic

CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune

CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease, an autoimmune or immune-mediated skin

CC disease, contact dermatitis, an allergic disease e.g. food

CC hypersensitivity, asthma, a transplantation associated disease, or a

CC chronic inflammatory demyelinating polynuropathy. Treating a PRO1031 or

CC degenerative cartilaginous disorder comprises administering a PRO1031 or

CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous

CC examples of the diseases and disorders are given in the specification.

XX

SO Sequence 1047 BP; 177 A; 381 C; 280 G; 209 T; 0 other;

QY

Query Match 100.0%; Score 1047; DB 22; Length 1047;

Best Local Similarity 100.0%; Pred. No. 8.6e-241;

Matches 1047; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 gccaggtgtgacagcgccgcccacgaagccacgtccgctgcgcacatgaagctcct 60

1 gccaggtgtgacagcgccgcccacgaagccacgtccgctgcgcacatgaagctcct 60

QY 61 ccccgccctcgtttctgacctggtgacacatgctgcgcacacatgacccctcct 120

61 ccccgccctcgtttctgacctggtgacacatgctgcgcacacatgacccctcct 120

DB 61 ccccgccctcgtttctgacctggtgacacatgctgcgcacacatgacccctcct 120

QY 121 cagggggacccccacagtcacagtcacacacacacacacacacacacacacac 180

121 cagggggacccccacagtcacagtcacacacacacacacacacacacacacac 180

DB 121 cagggggacccccacagtcacagtcacacacacacacacacacacacacacac 180

QY 181 cggcagagccccccac 240

181 cggcagagccccccac 240

DB 181 cggcagagccccccac 240

QY 241 agccctgtgtcagcgttgagagcagcagcagcagcagcagcagcagcagcagc 300

241 agccctgtgtcagcgttgagagcagcagcagcagcagcagcagcagcagcagc 300

DB 241 agccctgtgtcagcgttgagagcagcagcagcagcagcagcagcagcagcagc 300

QY 301 tacgaccagtcgcccgtgtcgtgcgcgagagagtggtgagagcagacacacacg 360

301 tacgaccagtcgcccgtgtcgtgcgcgagagagtggtgagagcagacacacacg 360

DB 301 tacgaccagtcgcccgtgtcgtgcgcgagagagtggtgagagcagacacacacg 360

QY 361 ctccatctacacctgagatgagtcgtgacagcagcagcagcagcagcagcagc 420

361 ctccatctacacctgagatgagtcgtgacagcagcagcagcagcagcagcagc 420

DB 361 ctccatctacacctgagatgagtcgtgacagcagcagcagcagcagcagcagc 420

QY 421 ggccttcgcagagtcgctgtgacagagcgtgtacagtcagcagcagcagcagc 480

421 ggccttcgcagagtcgctgtgacagagcgtgtacagtcagcagcagcagcagc 480

DB 421 ggccttcgcagagtcgctgtgacagagcgtgtacagtcagcagcagcagcagc 480

QY 481 tgcgtcctaactcgtgagcgtgtcctcagagcgtgtcgtgagcgcgcgcgcgtc 540

481 tgcgtcctaactcgtgagcgtgtcctcagagcgtgtcgtgagcgcgcgcgcgtc 540

DB 481 tgcgtcctaactcgtgagcgtgtcctcagagcgtgtcgtgagcgcgcgcgcgtc 540

QY 541 ccgagcagcgtcgaggctcccaacacacacacacacacacacacacacacacac 600

541 ccgagcagcgtcgaggctcccaacacacacacacacacacacacacacacacac 600

DB 541 ccgagcagcgtcgaggctcccaacacacacacacacacacacacacacacacac 600

QY 601 cgtcccgctgcgctgacacacacacacacacacacacacacacacacacacac 660

601 cgtcccgctgcgctgacacacacacacacacacacacacacacacacacacac 660

DB 601 cgtcccgctgcgctgacacacacacacacacacacacacacacacacacacac 660

QY 661 cccctagactgac 720

661 cccctagactgac 720

DB 661 cccctagactgac 720

QY 721 tattatagctcccccac 780

721 tattatagctcccccac 780

DB 721 tattatagctcccccac 780

QY 781 cagccccccac 840

781 cagccccccac 840

Db 781 cagcccccaactgtttctcctatctccagcctagtagtggtgtagaagagctcagc 840

Qy 841 acctcttccagcccttaaaagctgcagaaaaggtgtcacagggcttccgttacccttgctc 900  
 |||||

Db 841 acctcttccagcccttaaaagctgcagaaaaggtgtcacagggcttccgttacccttgctc 900  
 |||||

Qy 901 cctgtctgtctccggcttcccttaccctatcactgctcagggcccgagctgctc 960  
 |||||

Db 901 cctgtctgtctccggcttcccttaccctatcactgctcagggcccgagctgctc 960  
 |||||

Qy 961 ttcccaactctcttggaagttccctgtttcttaacaattatttaagtgtacgtgatt 1020  
 |||||

Db 961 ttcccaactctcttggaagttccctgtttcttaacaattatttaagtgtacgtgatt 1020  
 |||||

Qy 1021 attaacgtatgatacattccccaaaa 1047  
 |||||

Db 1021 attaacgtatgatacattccccaaaa 1047  
 |||||

RESULT 5  
 ID AAA58991 standard; CDNA; 1107 BP.  
 AC AAA58991;  
 DT 07-NOV-2000 (first entry)  
 DE cDNA encoding a human Interleukin (IL) 171 polypeptide.  
 KM Interleukin; IL-17; CTIA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
 XX IL-177; IL-171; cell proliferation; cancer; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 115..708  
 FT sig\_peptide 115..165  
 FT mat\_peptide 166..705  
 FT /\*tag= a  
 FT /\*tag= b  
 FT /\*tag= c  
 PN WO200042188-A2.  
 PD 20-JUL-2000.  
 PF 10-JAN-2000; 2000MO-US00006.  
 PR 11-JAN-1999; 99US-0228822.  
 PA (SCHE ) SCHERING CORP.  
 PI Gorman DM, Bazan JF, Kastelein RA;  
 DR WPI; 2000-466130/40.  
 DR P-PSDB; AAB07602.  
 XX New isolated polynucleotide encoding a mammalian Interleukin-17 like  
 PT protein used to identify genes for homologous proteins -  
 PS Disclosure; Page 20-21; 111pp; English.  
 XX The present sequence encodes an Interleukin-171 (IL-171) polypeptide.  
 CC The polypeptide is an IL-17-like (CTIA-8 related) protein. It is a  
 CC member of a new group of Interleukins, IL-170 polypeptides. The members  
 CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170  
 CC protein can be used to treat abnormal proliferation e.g. cancer  
 CC or degenerative conditions. Antibodies can be used in diagnostic  
 CC methods to detect over production of IL-170 protein in cells or body  
 CC fluids.  
 SQ Sequence 1107 BP; 183 A; 336 C; 306 G; 222 T; 0 other;

Query Match 98.2%; Score 1028.4; DB 21; Length 1107;  
 Best Local Similarity 99.8%; Pred. No. 2.4e-236;  
 Matches 1040; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 gccaggtgtcagagcgctccaaagccagcttcccgcttccgcacatagactcct 60  
 Db 66 gccaggtgtcagagcgctccaaagccagcttcccgcttccgcacatagactcct 125

Qy 61 ccccgctctctgtttctgacctgtgtgcacatagcttcccgcttccgcacatagactcct 120  
 Db 126 ccccgctctctgtttctgacctgtgtgcacatagcttcccgcttccgcacatagactcct 185

Qy 121 cagggggaccccccaagtaacgtaacccacatgctactcgtgtgagaaactgcccc 180  
 Db 186 cagggggaccccccaagtaacgtaacccacatgctactcgtgtgagaaactgcccc 245

Qy 181 cggccagggcccccccaactgtgtgtcgaaggtgcgaagtgaggagagcttgcctt 240  
 Db 246 cggccagggcccccccaactgtgtgtcgaaggtgcgaagtgaggagagcttgcctt 305

Qy 241 agccctgtgttccagcttgcagagcagcaagcgaaggggagcagagagccctcagc 300  
 Db 306 agccctgtgttccagcttgcagagcagcaagcgaaggggagcagagagccctcagc 365

Qy 301 taagaccaggtgccggtgtctgcgcggagaggtgtgttggaggaagaccaccacagc 360  
 Db 366 taagaccaggtgccggtgtctgcgcggagaggtgtgttggaggaagaccaccacagc 425

Qy 361 ctccatctacccttgagataccgtgttgacacagatagagaccgttccacaagaact 420  
 Db 426 ctccatctacccttgagataccgtgttgacacagatagagaccgttccacaagaact 485

Qy 421 ggccttcgcagagtgctctgtcagagagctgtatcgaatgcagagcggccgcagacagc 480  
 Db 486 ggccttcgcagagtgctctgtcagagagctgtatcgaatgcagagcggccgcagacagc 545

Qy 481 tgcgtcaactcgtgggctgtctccagaagcttctgtgtgtgcgcgcggcctgtc 540  
 Db 546 tgcgtcaactcgtgggctgtctccagaagcttctgtgtgtgcgcgcggcctgtc 605

Qy 541 ccgcagaggtctcgggcttccccaacacttgggaccttgccttccacacagagttcatca 600  
 Db 606 ccgcagaggtctcgggcttccccaacacttgggaccttgccttccacacagagttcatca 665

Qy 601 gctcccgctgtgactgacctgtgtctgcccgttcaatgtgacccggagagcggtggg 660  
 Db 666 gctcccgctgtgactgacctgtgtctgcccgttcaatgtgacccggagagcggtggg 725

Qy 661 cccctagactggaacagctgtctccccaagagcagccccattatgtgtattatgt 720  
 Db 726 cccctagactggaacagctgtctccccaagagcagccccattatgtgtattatgt 785

Qy 721 tattatatgctccccaacatacccttggggtctggtgacatcccgltcttgagga 780  
 Db 786 tattatatgctccccaacatacccttggggtctggtgacatcccgltcttgagga 845

Qy 781 cagcccccaactgtttctcctatctcactcagctcagtggttgaggaagagctcagc 840  
 Db 846 cagcccccaactgtttctcctatctcactcagctcagtggttgaggaagagctcagc 905

Qy 841 accttccagcccttaaaagctgcagaaaaggtgtcacagggcttccgttacccttgctc 900  
 Db 906 accttccagcccttaaaagctgcagaaaaggtgtcacagggcttccgttacccttgctc 965

Qy 901 cctgtctgtctccggcttcccttaccctatcactgctcagggcccgagctgctc 959  
 Db 966 cctgtctgtctccggcttcccttaccctatcactgctcagggcccgagctgctc 1025

Qy 960 ctcccaactctcttggaagtaacccctgtttcttaacaattatttaagtgtacgtgatt 1019  
 Db 1026 ctcccaactctcttggaagtaacccctgtttcttaacaattatttaagtgtacgtgatt 1085

OY 1020 tattaactgatacaacatcc 1041  
|||||  
Db 1086 tattaactgatacaacatcc 1107

RESULT 6  
AAA59149  
ID AAA59149 standard; cDNA; 1107 BP.

AC AAA59149;

DT 07-NOV-2000 (first entry)

DE cDNA encoding a human Interleukin-171 polypeptide.

XX Interleukin; IL-171; cytokine; CTA-8; IL-17; IL-175; IL-172; IL-173;  
XX IL-174; IL-176; IL-177; cell proliferation; cancer; ss.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 115..708

FT /\*tag= a /product= "interleukin-171"  
FT sig\_peptide 115..165

FT /\*tag= b  
FT mat\_peptide 166..705  
FT /\*tag= c

PN WO200042187-A1.

PD 20-JUL-2000.

PF 10-JAN-2000; 2000WO-US00005.

PR 11-JAN-1999; 99US-0229402.

PA (SCHE) SCHERING CORP.

PI Gorman DM, Bazan JF, Kastelein RA;

DR WPI: 2000-476060/41.  
DR P-PSDB; AAB07684.

PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
PT interleukin-171 (IL-171), useful for recombinant production of IL-171  
PT which can be used for treating conditions associated with abnormal  
PT physiology or development -

PS Claim 1; Page 10-11; 11pp; English.

XX The present sequence encodes an Interleukin (IL)-171 polypeptide. It  
CC is a mammalian homologue of the cytokine designated CTLA-8 (also  
CC referred to as IL-17). The specification also describes homologues  
CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
CC cDNA molecules which code for related or homologous proteins. The  
CC IL-171 protein, antibodies against IL-171, and compounds which have  
CC binding affinity to IL-171 are useful in treatment of conditions  
CC associated with abnormal physiology or development, including abnormal  
CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
CC The IL-171 protein can be used in kits and assay methods for identifying  
CC compounds that selectively bind to IL-171.

SO Sequence 1107 BP; 183 A; 396 C; 306 G; 222 T; 0 other;

Query Match 98.2%; Score 1028.4; DB 21; Length 1107;  
Best Local Similarity 99.8%; Pred. No. 2.4e-236;  
Matches 1040; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 gccaggtgtgacgagcgtcccaagccagcctgcgcgtgcgcacatgagctcct 60

Db 66 gccaggtgtgacgagcgtcccaagccagcctgcgcgtgcgcacatgagctcct 125

OY 61 ccccggtcctctgtttctgaacctggtgcacacatgcttgccacatgacctcct 120

Db 126 ccccggtcctctgtttctgaacctggtgcacacatgcttgccacatgacctcct 185

OY 121 cagggggcagcccccacagcgtgtaacccacatgcttctggtcgaagaatgcctc 180

Db 186 cagggggcagcccccacagcgtgtaacccacatgcttctggtcgaagaatgcctc 245

OY 181 cggcagagcccccacacatgctgtcgaaggtgcgaagtggggcaggtcttgctgt 240

Db 246 cggcagagcccccacacatgctgtcgaaggtgcgaagtggggcaggtcttgctgt 305

OY 241 agcctgtgtgtccagcgtggaagcagcaagggggaagcagcagagccctcagc 300

Db 306 agcctgtgtgtccagcgtggaagcagcaagggggaagcagcagagccctcagc 365

OY 301 tacgacccagtgccggtgtcgcgcgagagaggtgttggagggcagacccacagcg 360

Db 366 tacgacccagtgccggtgtcgcgcgagagaggtgttggagggcagacccacagcg 425

OY 361 ctccatctacccctgagagataccgtgtggaacagagatgagacccctacacagaagct 420

Db 426 ctccatctacccctgagagataccgtgtggaacagagatgagacccctacacagaagct 485

OY 421 ggccttcgcagagtgctgtgcagagagctgtatcgatgcagcagcggcgcgagaagc 480

Db 486 ggccttcgcagagtgctgtgcagagagctgtatcgatgcagcagcggcgcgagaagc 545

OY 481 tgcctcaactcctggtgagctgtctcagaagcctgtcgtggtgcgcgcgcgcgcgcgc 540

Db 546 tgcctcaactcctggtgagctgtctcagaagcctgtcgtggtgcgcgcgcgcgcgcgc 605

OY 541 ccgagagcgtcgtgggtcctccacacatggtggccttgctcctccacacagatctacca 600

Db 606 ccgagagcgtcgtgggtcctccacacatggtggccttgctcctccacacagatctacca 665

OY 601 ggtcccgctgagcgtcacctgcgtgtcgcgcgttcacgtgtgacgcgcagcgcgtgggg 660

Db 666 ggtcccgctgagcgtcacctgcgtgtcgcgcgttcacgtgtgacgcgcagcgcgtgggg 725

OY 661 cccctagactggaacgtgtgtctccacagagagaccccttatatgtatattatgt 720

Db 726 cccctagactggaacgtgtgtctccacagagagaccccttatatgtatattatgt 785

OY 721 tattatattgctcccccacacataaccttgggtgtcgtgacatcccgctgtctgagga 780

Db 786 tattatattgctcccccacacataaccttgggtgtcgtgacatcccgctgtctgagga 845

OY 781 cagcccccaactgttctctcaatctccacagcctcaagtgttgggtgtagaagatcagc 840

Db 846 cagcccccaactgttctctcaatctccacagcctcaagtgttgggtgtagaagatcagc 905

OY 841 accttccagccttaaaagctgcagaaagtgtcacacggtcgtgttactctggcgc 900

Db 906 accttccagccttaaaagctgcagaaagtgtcacacggtcgtgttactctggcgc 965

OY 901 cctgtcgtcctccggtcctccttaacctatacgtgcctcagc -cccgcagcgtcct 959

Db 966 cctgtcgtcctccggtcctccttaacctatacgtgcctcagc -cccgcagcgtcct 1025

OY 960 ctcccaactcctctggaagtaacctgttcttaacaataatttaagtgtat 1019

Db 1026 ctcccaactcctctggaagtaacctgttcttaacaataatttaagtgtat 1085

OY 1020 tattaactgatacaacatcc 1041

Db 1086 tattaactgatacaacatcc 1107

RESULT 7

AAZ36836  
 ID AAZ36836 standard; cDNA; 1067 BP.  
 AC AAZ36836;  
 DT 13-MAR-2000 (first entry)  
 DE Nucleotide sequence of human Interleukin-21.  
 XX  
 XX Human: Interleukin-22; IL-22; IL-21; immune system disorder;  
 KW immune cell chemotaxis; haematopoietic cell disorder;  
 KW haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;  
 KW respiratory problem; organ rejection; graft-versus-host disease; GVHD;  
 KW inflammation; hyperproliferative disorder; tissue regeneration;  
 KW embryonic stem cell differentiation; embryonic stem cell proliferation;  
 KW haematopoietic lineage; allergic asthma; ss  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 34..627  
 FT /tag= a  
 FT /product= "IL-21"  
 FT sig\_peptide 34..1060  
 FT /tag= b  
 FT sig\_peptide 34..87  
 FT /tag= c  
 XX  
 PN MO9961617-A1.  
 XX  
 PD 02-DEC-1999.  
 XX  
 PF 27-MAY-1999; 99MO-US11644.  
 XX  
 PR 29-MAY-1998; 98US-0087340.  
 PR 10-SEP-1998; 98US-0099805.  
 PR 30-APR-1999; 99US-0131965.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Ebner R;  
 XX  
 PI WPI: 2000-072622/06.  
 DR P-PSDB; AAF53892.  
 DR  
 XX Novel polynucleotides used to develop products for treating e.g. immune  
 PT disorders, blood disorders, autoimmune disorders, allergies,  
 PT inflammation, hyperproliferative disorders or infections  
 XX  
 PS Claim 8; Fig 6A-B; 170pp; English.  
 XX  
 CC The present sequence encodes a human Interleukin-21 (IL-21)  
 CC protein. The specification also describes IL-22 polynucleotides and  
 CC polypeptides. The IL-21 polynucleotide was isolated from a cDNA library  
 CC of apoptotic T-cells. IL-21 and IL-22 may be useful in treating  
 CC deficiencies or disorders of the immune system, by activating or  
 CC inhibiting the proliferation, differentiation, or mobilization  
 CC (chemotaxis) of immune cells, treating or detecting deficiencies  
 CC of haematopoietic cells, to modulate haemostatic or thrombolytic  
 CC activity, in treating or detecting autoimmune disorders, treating  
 CC asthma (particularly allergic asthma) or other respiratory problems,  
 CC to treat and/or prevent organ rejection or graft-versus-host disease  
 CC (GVHD), to modulate inflammation, to treat or detect hyperproliferative  
 CC disorders, to treat or detect infectious agents, to differentiate,  
 CC proliferate and attract cells, leading to the regeneration of tissues,  
 CC IL-21 and IL-22 may also increase or decrease the differentiation or  
 CC proliferation of embryonic stem cells and haematopoietic lineage, may  
 CC be used to modulate mammalian characteristics.  
 CC  
 SQ Sequence 1067 BP; 215 A; 371 C; 273 G; 206 T; 2 other;

Query Match 96.1%; Score 1006.4; DB 21; Length 1067;

Best Local Similarity 98.9%; Pred. No. 4, 4e-231;  
 Matches 1021; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY	17	gtctcaagccagcctgccccgctgcgcgcacacatgacgtctctcccgctctgttt	76
DB	1	gtctcaagccagcctgccccgctgcgcgcacacatgacgtctctcccgctctgttt	60
QY	77	ctgacctgctgacacatgctgccccacacatgacccctctctaggggggacccccac	136
DB	61	ctgacctgctgacacatgctgccccacacatgacccctctctaggggggacccccac	120
QY	137	agtaacggtacccccacacactgctactcgtgtaggaactgccccctggcagggccccc	196
DB	121	agtaacggtacccccacacactgctactcgtgtaggaactgccccctggcagggccccc	180
QY	197	cacctctgctgtaggaagtgccaaagtgggggacagcttgcctgtaacctggtgtccagc	256
DB	181	cacctctgctgtaggaagtgccaaagtgggggacagcttgcctgtaacctggtgtccagc	240
QY	257	ctggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	316
DB	241	ctggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	300
QY	317	gtgtgtcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc	376
DB	301	gtgtgtcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggcggc	360
QY	377	agatattcgtgtgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	436
DB	361	agatattcgtgtgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	420
QY	437	ctgtgcaagcgtgtatcgtatgacacgagcggcggcggcggcggcggcggcggcggcggc	496
DB	421	ctgtgcaagcgtgtatcgtatgacacgagcggcggcggcggcggcggcggcggcggcggc	480
QY	497	cggcgtctccagagcgt	556
DB	481	cggcgtctccagagcgt	540
QY	557	ctcccaacacgtgggctgt	616
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QY	617	acctgt	676
DB	601	acctgt	660
QY	677	gt	736
DB	661	gt	720
QY	737	ccaacactaccctgt	796
DB	721	ccaacactaccctgt	780
QY	797	tccatctccagcctcagtagtggggtagaaggagctcagacctctccagcctt	856
DB	781	tccatctccagcctcagtagtggggtagaaggagctcagacctctccagcctt	840
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QY	917	cttcccttaccctatcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagc	975
DB	901	cttcccttaccctatcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagcgtcagc	960
QY	976	gaagtaaccctgttcttaaacatatttaagtgtacgtgtatttaaacatgtatgaac	1035
DB	961	gaagtaaccctgttcttaaacatatttaagtgtacgtgtatttaaacatgtatgaac	1020
QY	1036	acaatccccaaaa 1047	



Db 1021 acaaaaaaaaaa 1032

RESULT 8

ID AA167878 standard; DNA; 1067 BP.

AC AA167878;

DT 13-MAR-2002 (first entry)

DE Human Interleukin (IL)-21 nucleotide sequence.

XX Interleukin; IL-21; IL-22; immunosuppressive; cytostatic; thrombolytic;

KW antinflammatory; antibacterial; gene therapy; human; ds.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT CDS 34..627

FT /tag= a

FT /product= "IL-21"

FT sig\_peptide 34..87

FT /tag= c

FT mat\_peptide 88..624

FT /tag= d

XX

PN US2001023070-A1.

XX

PD 20-SEP-2001.

XX

PF 08-DEC-2000; 2000US-0731816.

XX

PR 29-MAY-1998; 98US-087240P.

PR 30-APR-1999; 99US-131865P.

PR 09-DEC-1999; 99US-169837P.

PR 27-MAY-1999; 99US-0320713.

PR 27-MAY-1999; 99WO-US11644.

XX

PA (EBNE/) EBNER R.

PA (RUBE/) RUBEN S M.

PI Ebner R, Ruben SM;

XX

DR WPI: 2001-638470/73.

DR P-PSDB: AAC66121.

XX

PT New interleukin-21 and interleukin-22 polynucleotides and polypeptides,

PT useful for treating, preventing or diagnosing e.g. disorders of

PT hematopoietic cells, autoimmune disorders, or hyperproliferative

PT diseases

XX

PS Claim 2; Fig 6A-B; 87bp; English.

XX

CC The invention relates to novel human proteins designated interleukin

CC (IL)-21 and IL-22. The IL-21 and IL-22 polynucleotides can be used in

CC linkage analysis as a marker for those specific chromosome, in chromosome

CC mapping, to control gene expression through triple helix formation or

CC antisense DNA or RNA, in gene therapy, in identifying individuals from

CC minute biological samples, as an alternative to restriction fragment

CC length polymorphism (RFLP) analysis, as polymorphic markers for forensic

CC purposes, as molecular weight markers, or as diagnostic probes. IL-21 and

CC IL-22 polypeptides can be used to treat, prevent or diagnose diseases of

CC the immune system by activating or inhibiting the proliferation,

CC differentiation or mobilization of immune cells, disorders of

CC hematopoietic cells (e.g. ataxia, human immunodeficiency virus (HIV)

CC infection, anemia, thrombocytopenia), autoimmune disorders (e.g. Grave's

CC disease, systemic lupus erythematosus, ophthalmia), graft versus host

CC disease, inflammation, hyperproliferative disorders, or infectious

CC diseases. The polypeptides are useful for generating antibodies, which

CC can be used to treat, inhibit or prevent diseases or conditions

CC associated with aberrant expression and/or activity of IL-21 or IL-22.

CC The present sequence represents the full-length nucleotide sequence of

CC human IL-21.

XX

SO Sequence 1067 BP; 215 A; 371 C; 273 G; 206 T; 2 other:

Query Match 96.1%; Score 1006.4; DB 23; Length 1067;

Best Local Similarity 98.9%; Pred. No. 4.4e-231;

Matches 1021; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 17 gctccaagccagcctgcccgcctgcccagccacatgagcctctcccgctctgttt 76

DB 1 gctccaagccagcctgcccgcctgcccagccacatgagcctctcccgctctgttt 60

QY 77 ctgacctgtgctacacatgctgcccacacatgacccctccctcaaggagcccccac 136

DB 61 ctgacctgtgctacacatgctgcccacacatgacccctccctcaaggagcccccac 120

QY 137 agtcaagctacccacacactgtactctgctgtagaactgcccctcgccagcccccac 196

DB 121 agtcaagctacccacacactgtactctgctgtagaactgcccctcgccagcccccac 180

QY 197 caactgtgctcgaagtgccaaagtgggggcaagcttgcctgtagccctgtgtccagc 256

DB 181 caactgtgctcgaagtgccaaagtgggggcaagcttgcctgtagccctgtgtccagc 240

QY 257 ctggagagcagcaagccacaggggggagcagagagccctcagctagagcccaatggccg 316

DB 241 ctggagagcagcaagccacaggggggagcagagagccctcagctagagcccaatggccg 300

QY 317 gtgctgcgagccgagagagtgcttgagagcagacacccacagcgtccatctcaccttg 376

DB 301 gtgctgcgagccgagagagtgcttgagagcagacacccacagcgtccatctcaccttg 360

QY 377 agataccgtgtgacacaggaatgagacgcgtatccacagaagctgacctgcgcagtgac 436

DB 361 agataccgtgtgacacaggaatgagacgcgtatccacagaagctgacctgcgcagtgac 420

QY 437 ctgtgcagagagctgtatgacatgacagagagccgagacagctgagctcaactccgtg 496

DB 421 ctgtgcagagagctgtatgacatgacagagagccgagacagctgagctcaactccgtg 480

QY 497 cggctgctcacaagcctgctgtgtgtgcgcgcgcgcctgctcccgcaagcgtcgcgg 556

DB 481 cggctgctcacaagcctgctgtgtgtgcgcgcgcgcctgctcccgcaagcgtcgcgg 540

QY 557 ctccccaacactggggccttgctctccacacagagttcatccacgctccgctgcgtgc 616

DB 541 ctccccaacactggggccttgctctccacacagagttcatccacgctccgctgcgtgc 600

QY 617 acctggtgtgctcccgcttcaatgtgacccgcgagagcgtggggcccttagagctgac 676

DB 601 acctggtgtgctcccgcttcaatgtgacccgcgagagcgtggggcccttagagctgac 660

QY 677 gttgtctcccaagagagcccccctattatgttatattattattattattattattatt 736

DB 661 gttgtctcccaagagagcccccctattatgttatattattattattattattattatt 720

QY 737 ccaacactaccccttgggtgtggaattcccggtgtctgagagaaagcccccactgttc 796

DB 721 ccaacactaccccttgggtgtggaattcccggtgtctgagagaaagcccccactgttc 780

QY 797 tcttatctccagagcccaatgtagtgggttaagaagatgagacacttcttcaagccct 856

DB 781 tcttatctccagagcccaatgtagtgggttaagaagatgagacacttcttcaagccct 840

QY 857 aaagctcagaanaaggtgacacagcgtctcgtaactgtgctccctgtcgtcccg 916

DB 841 aaagctcagaanaaggtgacacagcgtctcgtaactgtgctccctgtcgtcccg 900

QY 917 ctcccttaacctatcaactgtgcctcaag-ccccgaagcgtgcctcttcccaactccttg 975

DB 901 ctcccttaacctatcaactgtgcctcaag-ccccgaagcgtgcctcttcccaactccttg 960

Query Match	88.2%	Score 923.4	DB 22	Length 1177
Best Local Similarity	99.8%	Pred. No. 3,1e-211		
Matches 935	Conservative	0	Mismatches 1	Indels 1
			Gaps 1	
SO	Sequence 1177 BP: 206 A; 421 C; 334 G; 216 T; 0 other;			
CC	and chronic inflammation such as rheumatic diseases, graft versus host			
CC	disease and multiple sclerosis. IL-17 like antagonists are useful for			
CC	treating and preventing inflammatory disease, autoimmune disease,			
CC	allergies, asthma and organ or graft rejection in a patient and also			
CC	for inhibiting T cell proliferation and/or activation, in vivo B cell			
CC	proliferation or immunoglobulin secretion, and for blocking the effects			
CC	of IL-17 in inducing bone destruction. IL-17 like molecule is useful in			
CC	gene therapy and for mapping the location of the IL-17 like gene and			
CC	related genes on chromosomes, as hybridisation probes in diagnostic			
CC	assays. Non human animals in which the promoter for one or more of IL-17			
CC	like protein is either activated or inactivated are useful for drug			
CC	candidate screening. The present sequence is a cDNA encoding human IL-17			
CC	like protein.			
XX				
XX				
QY	53 agcgcctccccgcgcctctgtttcttgagccctgctgcagacaatgctgcccacacatgac	112		
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QY	236 aggcctccccgcgcgcctctgtttcttgagccctgctgcagacaatgctgcccacacatgac	295		
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QY	113 cctctccctcaagggggcaaccccaacagtlacagtlacccacactgctactcgtctagagaa	172		
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QY	296 cctctccctcagggggcaaccccaacagtlacagtlacccacactgctactcgtctagagaa	355		
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QY	476 cccctcagctacagaccacagctgcgcgtgtctgcggccggagggagtggtttgagagcagacac	535		
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Db				
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Db				





XX	Glasebrook AL, Su EW, Wei J, Liu L,
PI	
XX	WPI; 2000-303778/26.
DR	P-PSDB; AAY92238.
DR	
XX	
XX	Nucleic acid encoding an interleukin-17 (IL-17) homolog polypeptide
PT	which enhances hematopoiesis, useful for treating e.g. anemia,
PT	thrombocytopenia, viral and bacterial infections
XX	
PS	Claim 6; Page 92; 11pp; English.
XX	
CC	Interleukin 17 (IL-17) stimulates hematopoiesis and production of
CC	neutrophils, granulocytes, or platelets, this may be useful during
CC	chemotherapy. IL-17 homologues have at least one actively selected
CC	from induction of cytotoxic T cells, induction of lymphokine-activated
CC	killer cell proliferation or a B or T cell stimulation. The IL-17
CC	homologue may also be used to treat viral or bacterial infections,
CC	immune related diseases, anemia, leukemia, thrombocytopenia, uremia,
CC	Von Willebrand disease, postoperative cardiovascular dysfunction,
CC	treatment of AIDS (acquired immune deficiency syndrome)-related bone
CC	marrow failure, and inflammatory diseases of the gastrointestinal
CC	system, joints, and lungs.
XX	
XX	Sequence 591 BP; 91 A; 223 C; 179 G; 98 T; 0 other.

Query Match	Score	DB	Length
56.4%	591	21	591
100.0%	745	133	745

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Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

## RESULT 13

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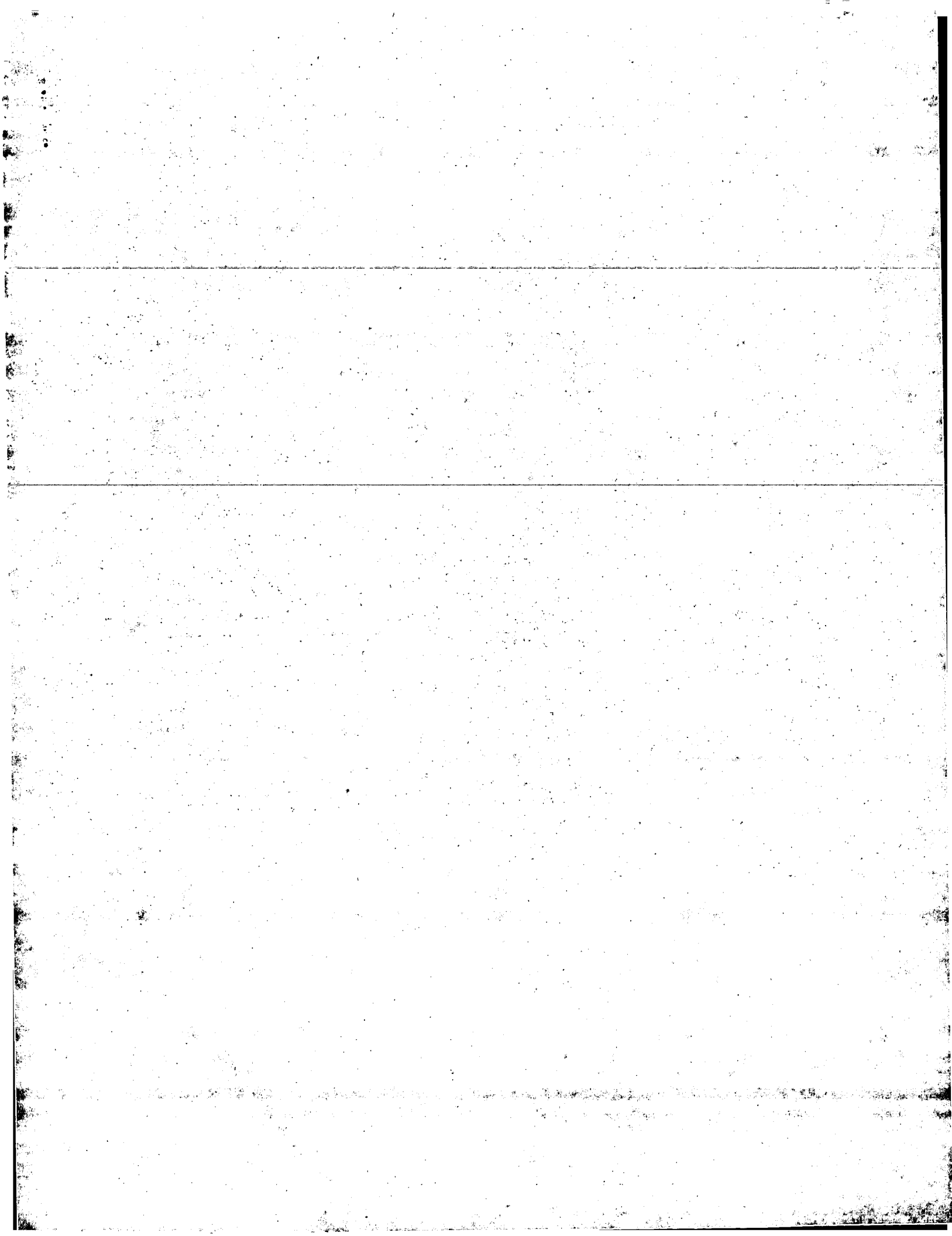
AAAS8990
ID   AAAS8990 standard; cDNA: 521 BP.
AC   AAAS8990;
DT   07-NOV-2000 (first entry)
XX
DE   cDNA encoding a human interleukin (IL) 171 polypeptide.
KW   Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
XX   IL-177; IL-171; cell proliferation; cancer; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1..372
FT     /tag="a
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XX
XX   WO200042188-A2.
XX
XX   20-JUL-2000.
XX
XX   10-JAN-2000; 2000WO-US00006.
XX
XX   11-JAN-1999; 99US-0228822.
XX
XX   (SCHE ) SCHERING CORP.
XX
XX   Gorman DM, Bazan JF, Kastelein RA;
XX
XX   WPI: 2000-466130/40.
XX
XX   P-PSDB: AAB07601.
XX
XX
XX   New isolated polynucleotide encoding a mammalian interleukin-17 11kx
XX   protein used to identify genes for homologous proteins -
XX
XX   Disclosure: Page 19-20; 11pp; English.
XX
XX
XX   The present sequence encodes an interleukin-171 (IL-171) polypeptide.
XX   The polypeptide is an IL-17-1like (CTLA-8 related) protein. It is a
XX   member of a new group of interleukins, IL-170 polypeptides. The members
XX   comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
XX   protein can be used to treat abnormal proliferation e.g. cancer
XX   or degenerative conditions. Antibodies can be used in diagnostic
XX   methods to detect over production of IL-170 protein in cells or body
XX   fluids.
XX
XX   Sequence 521 BP; 92 A; 165 C; 148 G; 116 T; 0 other;
SO

```

[illegible]









GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2002, 23:55:32 ; Search time 48.15 Seconds  
(without alignments)  
5341.190 Million cell updates/sec

Title: US-09-854-280-4  
Perfect score: 1047  
Sequence: 1 gccacggtgtcagcgccgtc.....tgatgacacatccccaacaa 1047

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
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5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58.2	5.6	7218	1 US-08-232-463-14	Sequence 14, Appl
2	45.8	4.4	152331	3 US-09-128-155-16	Sequence 16, Appl
3	44.6	4.3	1578	1 US-08-681-129-1	Sequence 1, Appl
4	42.4	4.0	291	4 US-08-931-858E-201	Sequence 201, App
5	42.4	4.0	291	4 US-08-931-858E-202	Sequence 202, App
6	42.4	4.0	471	4 US-08-931-858E-205	Sequence 205, App
7	42.4	4.0	471	4 US-08-931-858E-206	Sequence 206, App
8	41.2	3.9	2588	2 US-08-796-414B-6	Sequence 6, Appl
9	40.8	3.9	291	4 US-08-931-858E-199	Sequence 199, App
10	40.8	3.9	291	4 US-08-931-858E-200	Sequence 200, App
11	40.8	3.9	471	4 US-08-931-858E-203	Sequence 203, App
12	40.8	3.9	471	4 US-08-931-858E-204	Sequence 204, App
13	40.8	3.9	3695	1 US-08-091-569-1	Sequence 1, Appl
14	40.8	3.9	3695	1 US-08-203-676-1	Sequence 1, Appl
15	40.8	3.9	3695	2 US-08-822-238-1	Sequence 1, Appl
16	40.8	3.8	319	4 US-09-165-264-14	Sequence 14, Appl
17	39.6	3.8	320	4 US-09-165-264-14	Sequence 14, Appl
18	39.4	3.8	5115	3 US-08-348-518C-3	Sequence 3, Appl
19	39.4	3.8	5115	3 US-08-476-509B-3	Sequence 3, Appl
20	38.8	3.7	267	4 US-08-931-858E-222	Sequence 222, App
21	38.6	3.7	5822	3 US-08-899-595-4	Sequence 4, Appl
22	38.6	3.7	5822	3 US-08-899-595-5	Sequence 5, Appl
23	38.6	3.7	71989	4 US-09-443-501A-2	Sequence 2, Appl
24	38.2	3.6	1659	3 US-09-083-351-3	Sequence 3, Appl
25	38.2	3.6	1659	4 US-09-083-352-3	Sequence 3, Appl
26	38.2	3.6	3946	3 US-09-083-351-1	Sequence 1, Appl
27	38.2	3.6	3946	4 US-09-083-352-1	Sequence 1, Appl

28	38	3.6	1271	4 US-09-231-227-1	Sequence 1, Appl
29	37.8	3.6	318	4 US-09-165-264-12	Sequence 12, Appl
30	37.8	3.6	320	4 US-09-165-264-13	Sequence 13, Appl
31	37.8	3.6	822	4 US-09-228-986-38	Sequence 38, Appl
32	37.6	3.6	320	4 US-09-165-264-7	Sequence 7, Appl
33	37.4	3.6	320	4 US-09-165-264-11	Sequence 11, Appl
34	37.4	3.6	405	2 US-08-903-800A-3	Sequence 3, Appl
35	37	3.5	12001	1 US-08-458-568A-11	Sequence 11, Appl
36	37	3.5	44377	2 US-08-804-227C-7	Sequence 7, Appl
37	37	3.5	68750	3 US-09-335-409-1	Sequence 1, Appl
38	37	3.5	68750	3 US-09-568-102-1	Sequence 1, Appl
39	37	3.5	68750	4 US-09-567-969-1	Sequence 1, Appl
40	37	3.5	68750	4 US-09-568-480-1	Sequence 1, Appl
41	37	3.5	68750	4 US-09-568-486-1	Sequence 1, Appl
42	37	3.5	68750	4 US-09-568-472-1	Sequence 1, Appl
43	37	3.5	68750	4 US-09-568-472-2	Sequence 1, Appl
44	36.8	3.5	2580	3 US-09-050-863-2	Sequence 2, Appl
45	36.8	3.5	2580	4 US-09-359-081-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHERFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)636-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-F15  
US-08-232-463-14

[illegible]

Query Match	4.3%	Score 44.6	DB 1	Length 1578
Best Local Similarity	46.7%	Pred. No. 0.029		
Matches 177	Conservative	0	Mismatches 199	Indels 3
			Gaps	1
QY 242	gcccttggtgccagctgtgagcagcaagcagcaggggagcagcagagagcccttagct	301		
Db 457	GGTTGGTGTAGCGCCGTACACAGGCGCTTCCGCGTGGTGACAGGGGTACCTCTCCGAG	516		
QY 302	acgaaccagtcgcgggtgctcgccgagcagagagtgcttgtaggcagacaccacacagcgc	361		
Db 517	CTGCCACGCTCGCTCAGAGTGTCTGACGAGGGGGCTTTTACGACGAMTCCCGCGCTGCC	576		
QY 362	tccatctaaccttgtagataccggtgtgacacagcagatagagaccgcgtatccaaagaagctg	421		
Db 577	CC---CCGCTCAGGCGGACACCGCCGCGCCCTGTGTTGTAAGGCGGCGCGGG	633		



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,858E

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971486
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-931-858E-206

Query Match          4.0%; Score 42.4; DB 4; Length 471;
Best Local Similarity 55.4%; Pred. No. 0.068; Mismatches 66; Indels 0; Gaps 0;
Matches      82; Conservative    0; Mismatches     66; Indels    0; Gaps    0;

QY   410 ccacgaagctgctgcgttcgcagatgacctgtgcagaagcgtgatcatgacagcacggcg 469
       ||||| | | | | | ||||| | | | | | ||||| | | | | | |||||
DB   8 CCACAGCCCGACGAGCCGCCCGACGAGCTGGGGCACGCCGCTGCACACGGTGGCGTCATCG 67
QY   470 ccgcgacagcgtgcgtcaactcgtlccgctgcgtccagagcgtctgltgttgcgccg 529
       || | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB   68 AGGAAGCCCACTCGTGTAAGCATGTGGCCGCGACAGAGGCCCGCCCGTGGCTGGCCC 127
QY   530 cgagccctgctccgcgcagcagcgtcggcg 557
       ||||| | | | | | | | | | | | | | | | | | | | | | |
DB   128 TGGCCCTGCAGCCGGGCGCACGCCCGACGCG 155

RESULT      8
US-08-796-41AB-6
Sequence 6, Application US/0879641AB
Patent No. 5876987
GENERAL INFORMATION:
APPLICANT: Wendy C. Champness, Paul Brian
APPLICANT: and Todd B. Anderson
TITLE OF INVENTION: METHOD, DNA AND BACTERIA
TITLE OF INVENTION: FOR HYPERPRODUCTION OF AN
TITLE OF INVENTION: ANTIBIOTIC DUE TO
TITLE OF INVENTION: DISRUPTION OF AN AbsA
GENE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
COMPUTER: Acer

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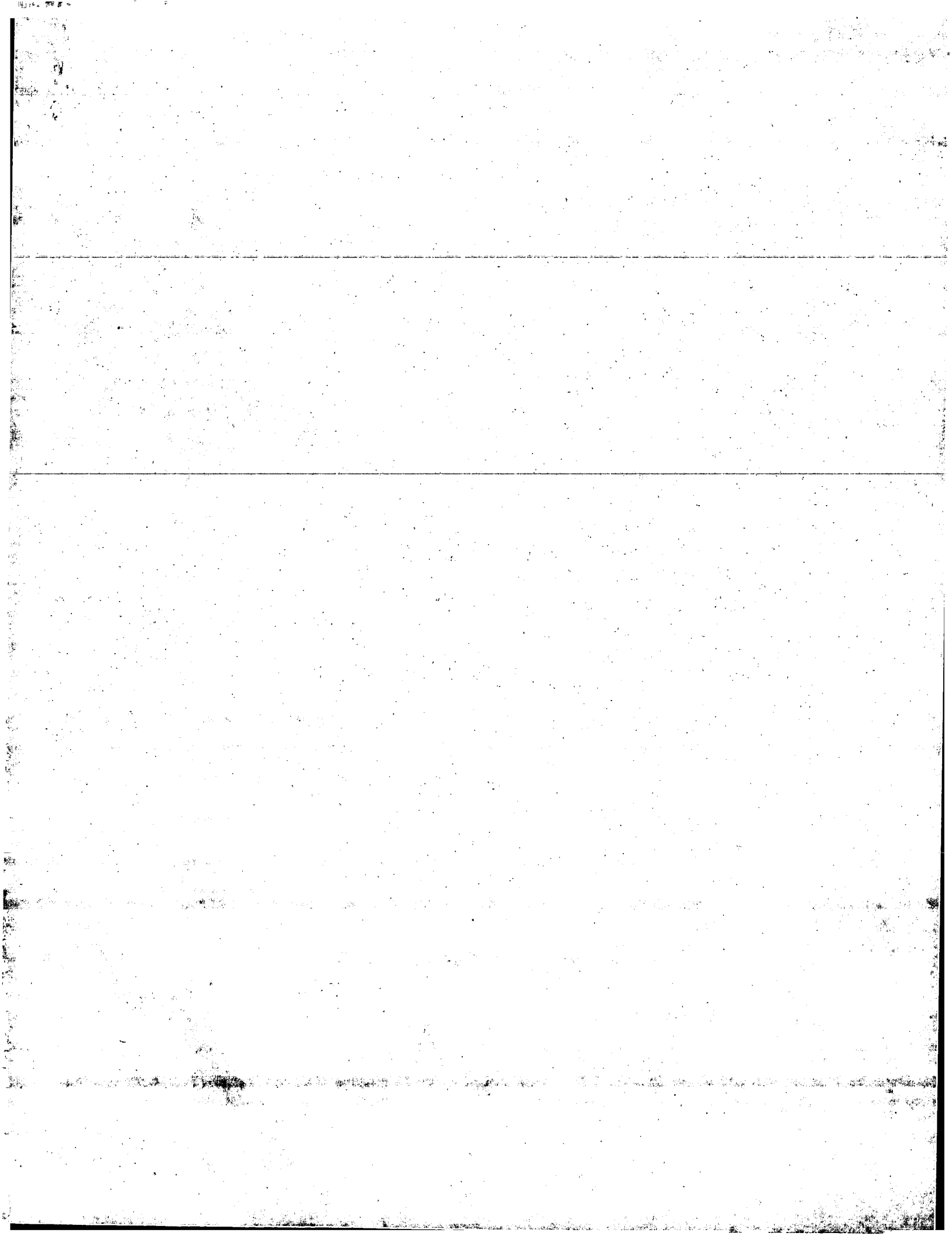


CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750,081  
FILING DATE: 27-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16777/149/ALLEN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109

Search completed: September 4, 2002, 01:47:21  
Job time: 6709 sec







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 3, 2002, 23:50:42 ; Search time 1611.71 Seconds  
(without alignments)  
8767.900 Million cell updates/sec

Title: US-09-854-280-4  
Perfect score: 1047  
Sequence: 1 gccaggtgycagcgcgcgc.....tgatgaacacatcccaaaa 1047

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	377	36.0	669	12 AG139411	AG139411 Pan trogl
C 2	244.8	23.4	264	10 BE551188	BE551188 7b55903.x
C 3	66	6.3	1203	12 CNS01574	AL106054 Drosophila
C 4	58.6	5.6	873	12 AG043471	AG043471 Pan trogl
C 5	58	5.5	1452	12 AG032979	AG032979 Pan trogl
C 6	56.8	5.4	441	9 AI275406	AI275406 q163c10.x
C 7	56.8	5.4	836	10 B1828970	B1828970 603074846
C 8	56.4	5.4	1520	12 AG057334	AG057334 Pan trogl
C 9	55.8	5.3	932	12 CNS00720	AL065742 Drosophila
C 10	55.6	5.3	925	12 CNS0091P	AL053013 Drosophila
C 11	55.2	5.3	524	9 AI430337	AI430337 m168b10.y
C 12	55.2	5.3	718	10 B1561289	B1561289 603256441
C 13	54.8	5.2	1137	10 BG809979	BG809979 mgct002xd
C 14	54.6	5.2	925	12 CNS0091P	AL053013 Drosophila
C 15	54.4	5.2	862	12 AG036151	AG036151 Pan trogl
C 16	52.6	5.0	435	10 BG579143	BG579143 df23f12.y
C 17	52.6	5.0	673	9 AL577596	AL577596 AL577596

18	52.6	5.0	844	12 CNS0052P	AL056652 Drosophila
19	52.2	5.0	1025	12 CNS031M	AL249701 Tetradon
20	51.6	4.9	1203	12 CNS01574	AL106054 Drosophila
C 21	51.4	4.9	935	12 CNS006X	AL066051 Drosophila
C 22	51.2	4.9	910	12 AG032931	AG032931 Pan trogl
C 23	50.8	4.9	832	12 AG133251	AG133251 Pan trogl
C 24	50.8	4.9	989	12 AG030675	AG030675 Pan trogl
C 25	50.6	4.8	1081	9 AW727480	GA_Ea001
C 26	50.4	4.8	1101	12 CNS00397	AL063912 Drosophila
C 27	50.2	4.8	868	3 B1644484	OP2219 M1
C 28	50.2	4.8	957	10 BM416095	OP21179 M
C 29	50.2	4.8	1077	12 CNS0156Q	AL105068 Drosophila
C 30	50	4.8	844	12 CNS0052P	AL056652 Drosophila
C 31	49.4	4.7	420	10 W88186	m168b10.y
C 32	49.4	4.7	538	9 AL514267	AL514267
C 33	49.2	4.7	1124	12 AG041123	AG041123 Pan trogl
C 34	49	4.7	664	12 BH140735	BH140735
C 35	49	4.7	839	12 CNS0040B	AL054280 Drosophila
C 36	49	4.7	840	12 B19033	B19033 T28M6-Sp6 T
C 37	49	4.7	848	12 AG060231	AG060231 Pan trogl
C 38	49	4.7	993	12 AG090948	AG090948 Pan trogl
C 39	49	4.7	1030	12 AG077951	AG077951 Pan trogl
C 40	48.8	4.7	724	12 AG171201	AG171201 Pan trogl
C 41	48.8	4.7	869	12 AG162064	AG162064 Pan trogl
C 42	48.8	4.7	952	12 CNS0766T	AL431019 T7 end of
C 43	48.6	4.6	388	10 BG909378	BG909378 Talc1102C
C 44	48.6	4.6	421	12 BH254057	BH254057 SALC11059
C 45	48.4	4.6	744	12 CNS0172K	AL108698 Drosophila

## ALIGNMENTS

RESULT 1  
AG139411/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
PRIMERS  
SEQUENCING: -21M13  
LIBRARY  
VECTOR : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers  
1. 669  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="PTB-153006.F"

AG139411 669 bp DNA linear GSS 04-NOV-2001  
Pan troglodytes DNA, clone: PTB-153006.F, genomic survey sequence.  
AG139411.1 GI:1666089  
GSS: GSS (genome survey sequence).  
Pan troglodytes male lymphoblast DNA, clone: lib:PTB Chimpanzee Male  
BAC library clone: PTB-153006.F.  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
1 (sites)  
Tokohi, Y., Watanabe, H. and Sakaki, Y.  
BAC end sequences of library PTB  
Unpublished  
2 (bases 1 to 669)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Tokohi, Y., Watanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimpanzee@sc.riken.go.jp, URL: http://ngp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI  
Location/Qualifiers  
1. 669  
/organism="Pan troglodytes"  
/db\_xref="taxon:9598"  
/clone="PTB-153006.F"

/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTM Chimpanzee Male BAC library"  
BASE COUNT 143 a 220 c 203 g 100 t 3 others  
ORIGIN

Query Match 36.0%; Score 377; DB 12; Length 669;  
Best Local Similarity 90.6%; Pred. No. 1.3e-65;  
Matches 423; Conservative 0; Mismatches 42; Indels 2; Gaps 2;

QY 410 ccacgaagctgcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 468  
DB 505 ccacgaagctgcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 446  
QY 469 ccgagagacagctgcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 528  
DB 445 ccgagagacagctgcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 387  
QY 529 ccgagagacagctgcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 588  
DB 386 ccgagagacagctgcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 327  
QY 589 ccagcttccacagctgcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 648  
DB 326 ccagcttccacagctgcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 267  
QY 649 gagagcgtgagcccttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 708  
DB 266 gagagcgtgagcccttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 207  
QY 709 tgatattatgttattatgtcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 768  
DB 206 tgatattatgttattatgtcttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 147  
QY 769 gtgtctgagagacagcccttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 828  
DB 146 gtgtctgagagacagcccttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 87  
QY 829 aagagagctgagcccttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 875  
DB 86 aagagagctgagcccttgcgcgagtgcc-tgtgcaagctgtatcgaatgacgagcgg 40

RESULT 2  
BE551188/c 264 bp mRNA linear EST 10-AUG-2000  
LOCUS BE551188  
DEFINITION 7b55g03.x1 NCI CGAP Ju24 Homo sapiens CDNA clone IMAGE:3232180 3'  
ACCESSION BE551188  
VERSION BE551188.1 GI:9792880  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 264)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP).  
JOURNAL Tumor Gene Index  
COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMW, send email to:  
[info@image.llnl.gov](mailto:info@image.llnl.gov)  
Seq primer: -400p from Gibco  
High quality sequence stop: 259.

## FEATURES

source

Location/Qualifiers  
1. 264  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NCI-CGAP\_Ju24"  
/issue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
modified polylinker; Plasmid DNA from the normalized  
library NCI CGAP Ju24 was prepared, and ss circles were  
used as tracer in a subtractive hybridization reaction.  
The driver was PCR-amplified cDNAs from a pool of 5,000  
clones made from the same library (clonids  
1414920-1417991 and 1520904-1522439). Subtraction by Bento  
Soares and M. Fatima Bonaldo."

BASE COUNT 66 a 50 c 88 g 60 t  
ORIGIN

Query Match 23.4%; Score 244.8; DB 10; Length 264;  
Best Local Similarity 98.8%; Pred. No. 3.4e-39;  
Matches 257; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 780 acagccccacgtgtctctctatctccagctcagtagtgagggtagaagagctcaag 839  
DB 264 acagccccacgtgtctctctatctccagctcagtagtgagggtagaagagctcaag 205  
QY 840 caactctccagcccttaagctgcagaaaggtgtcacagcgtgcctgtaccttgct 899  
DB 204 caactctccagcccttaagctgcagaaaggtgtcacagcgtgcctgtaccttgct 145  
QY 900 cccctgtccctcccggtctccctaccctaccctaccctaccctaccctaccctaccct 958  
DB 144 cccctgtccctcccggtctccctaccctaccctaccctaccctaccctaccctaccct 85  
QY 959 tcttcccaacctccttggaagacccctgttcttaacaattatttaagtagtctgta 1018  
DB 84 tcttcccaacctccttggaagacccctgttcttaacaattatttaagtagtctgta 25  
QY 1019 ttattaaactgtagaacaca 1038  
DB 24 ttattaaactgtagaacaca 5

RESULT 3  
CNS015Y4/c 1203 bp DNA linear GSS 26-JUL-1999  
LOCUS CNS015Y4/c  
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC  
BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
ACCESSION AL106054.1 GI:5619805  
VERSION AL106054.1 GI:5619805  
KEYWORDS GSS.  
SOURCE fruit fly.  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 1203)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage;  
BP 191 91006 EVRY cedex - FRANCE (E-mail: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))

COMMENT - Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
<http://www.edgp.ebi.ac.uk>. This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billand at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector



ORGANISM	TITLE	JOURNAL	REFERENCE
BAC library clone: PTB-007004.F. Pan troglodytes			
Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Primates; Catarrhini; Hominoidea; Pan.			
1 (sites)			
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totochi, Y., Watanabe, H. and Sakaki, Y.			
BAC end sequences of Library PTB Unpublished			
2 (bases 1 to 1452)			
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totochi, Y., Watanabe, H. and Sakaki, Y.			
Direct Submission			
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho; Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: shimbudgsc@riken.go.jp, URL: http://nyp.gsc.riken.go.jp/, Tel.:81-45-503-9111, Fax:81-45-561-9170)			
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.			
PRIMERS			

FEATURES	Location/Qualifiers
source	1. .1452

BASE COUNT	ORIGIN
23 a	581 c
600 g	74 t
	174 others

Query Match	5.5%;	Score 58;	DB 12;	Length 1452;
Best Local Similarity	46.3%;	Pred. No. 0.089;		
Matches 304;	Conservative	0;	Mismatches 339;	Indels 14;
				Gaps 4

[illegible]

D<sub>b</sub> 1129 GCGGGCCGCGCGGGNCCGGGGGCCCGCGGCAGCGCGGNCCGGGCCCGCCGCGCCCCC 1188  
Q<sub>y</sub> 481 t-----gcgtcaactcgttgcgagctgtctccagagacctgtctgtgtcgacgcggcg 534  
D<sub>b</sub> 1189 NCGGCGCGCGCGCGCGCCCGCGCGCNCGGGCGCGCCNCGCGCGCGCGCGCGCGCGCGCGCN 1248  
Q<sub>y</sub> 535 ctgtctccgcgcgacgagctcgcggatccccacaacttgaggctttgccttcacaccgagtt 594  
D<sub>b</sub> 1249 CGCGCGCGCGCGGCMCA 1308  
Q<sub>y</sub> 595 catcacgltcccgcgttcgctgcacactgtcgttgcgccgtlcatgttacgcgcgag 651  
D<sub>b</sub> 1309 TCNCNCNCNCGGGGCMCCGCG 1365

RESULT	-6				
LOCUS	A1275406				
DEFINITION	A1275406 441 bp mRNA linear EST 29-JAN-1999 gi63c10.x1 Soares_NHMPU_S1 Homo sapiens cDNA IMAGE:1877010 3' similar to contains TARI.B1 TARI repetitive element ; mRNA sequence.				
ACCESSION	A1275406				
VERSION	A1275406.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 441)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: c9abbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1146 Std Error: 0.00  
Seq primer: -400P from Glibco  
High quality sequence stop: 428.  
Location/Qualifiers  
1. 441  
FEATURES  
source

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1877010"  
 /clone\_lib="Soares\_NbHMFu\_S1"  
 /tissue\_type="Pooled human melanocyte, fetal heart, and  
 pregnant uterus"  
 /lab\_host="DH10B"  
 /note="Organ: mixed (see below); Vector: p7773D-Pac  
 (Pharmacia) with a modified polylinker; Site.1: Not I;  
 Site.2: Eco RI; Equal amounts of plasmid DNA from three  
 normalized libraries (melanocyte 2NbH, pregnant uterus  
 NbHfu, and fetal heart NbHf19w) were mixed, and ss circles  
 were made in vitro. Following HAP purification, this DNA  
 was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from pools of  
 5,000 clones made from the same 3 libraries. The pools  
 consisted of I.M.A.G.E. clones 260232-265223,  
 340488-345479, and 484488-489479."

	Query Match	5.48;	Score 56.8;	DB 9;	Length 441;
	Best Local Similarity	51.28;	Pred. No. 0.14;		
	Matches 133;	Conservative	0;	Mismatches 127;	Indels 0;
				Gaps	
QY	349	caccacacagcgtccatcttcacccctggagatacgcgtgtggacacgagatgagaccgcta	408		
Db	152	caccacacttcggcagcgtgtgcgccttcggcgttcacaaatctcttacgaccctccgacgagta	211		
QY	409	tccacagaagcttgccttcgcgcagatgtccctgttgcagaagcgttcatatgcacgcagagcg	468		

```

Db 212 CCCAGGATACCTGCTGAAGCTTACTGCTGCGGGGCTCCAGACCGGGCTTTCGG 271
Oy 469 ccgagagacagctgctgctcaactcgtgctgctgctcagagcctgcgtgctgctgctg 528
Db 212 CGAGAGAGACGCGCTTCCGAGCGCCCTGTCTACATGCCCCACCGCTGCTCCTCGCG 331
Oy 529 ccgagcctgctcccgagagcgtcgggggtcccccacacctgaggccttgccttcacac 588
Db 332 CACCCCGCGCTGCGCGCGCGCGCGCTTCGCTACACGAGCGCTACGTACCATCCCGT 391
Oy 589 cgagttcattccagctcccg 608
Db 392 GGGCTGACACTGCTGCTCCCG 411

RESULT 7
Bi828970 836 bp mRNA linear EST 04-OCT-2001
LOCUS 603074846F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5166851 5'
DEFINITION mRNA sequence.
ACCESSION Bi828970
VERSION Bi828970.1 GI:15940520
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 836)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNL414 row: k column: 12
High quality sequence stop: 748.
Location/Qualifiers
1..836
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5166851"
/clone_id="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is Oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb. Insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
BASE COUNT 158 a 293 c 246 g 139 t
ORIGIN
Query Match 5.4%; Score 56.8; DB 10; Length 836;
Best Local Similarity 51.2%; Pred. No. 0.15;
Matches 133; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

Oy 349 caccacacagctcattacacctgagatagcgtgtgacagagatgagaccgcta 408
Db 34 CACCAACTGTGGCGACGCTGCTGCGCTTCCGAGCGCTTCCTACAGACCGCGAGGTA 93
Oy 409 tcacagagctgcttcgcagagtgctgtcagagcgtatcgtatgcagcagcgg 468

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Db 94 CCCAGGATACCTGCTGAAGCTTACTGCTGCGGGGCTCCAGACCGGGCTTTCGG 153
Oy 469 ccgagagacagctgctgctcaactcgtgctgctgctcagagcctgcgtgctgctgctg 528
Db 154 CGAGAGAGACGCGCTTCCGAGCGCCCTGTCTACATGCCCCACCGCTGCTCCTCGCG 213
Oy 529 ccgagcctgctcccgagagcgtcgggggtcccccacacctgaggccttgccttcacac 588
Db 214 CACCCCGCGCTGCGCGCGCGCGCGCTTCGCTACACGAGCGCTACGTACCATCCCGT 273
Oy 589 cgagttcattccagctcccg 608
Db 274 GGGCTGACACTGCTGCTCCCG 293

RESULT 8
AG057334 1520 bp DNA linear GSS 02-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-043006.R, genomic survey sequence.
DEFINITION AG057334
ACCESSION AG057334
VERSION AG057334.1 GI:16594793
KEYWORDS GSS; GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphoblast DNA, clone_1lb:PTB Chimpanzee Male
BAC Library clone:PTB-043006.R.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE 1 (sites)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totochi,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1520)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totochi,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Aseo Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suenho-chou,Tsukuba-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpses@sc.riken.go.jp, URL:http://ngp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the Rad process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..1520
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone_image="PTB-043006.R"
/sex="male"
/cell_type="lymphoblast"
/clone_id="PTB Chimpanzee Male BAC Library"
BASE COUNT 97 a 644 c 625 g 50 t 104 others
ORIGIN
Query Match 5.4%; Score 56.4; DB 12; Length 1520;
Best Local Similarity 44.0%; Pred. No. 0.19;
Matches 287; Conservative 0; Mismatches 361; Indels 4; Gaps 1;

Oy 35 ccgctgctgctcaccatgacgtctctcccgccctcgtttcttactggtgtcacaca 94
Db 751 CCCGCGCGCGGAGAGACGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 810
Oy 95 tgcctgctcaccacagacctccctcctcaggggaccccccacagctcaggtaccacac 154

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COMMENT	REFERENCE	AUTHORS	JOURNAL	TITLE	ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT	
											9	
											CNS00720/c	
											9	
											CNS00720	
											932 bp	
											DNA	
											linear	
											GSS 03-JUN-1999	
											BACR14B09 of RPc1-98 library from <i>Drosophila melanogaster</i> (fruit fly), genomic survey sequence.	
											AT066742	
											AT066742	
											GI:4945205	
											GSS	
											fruit fly.	
											<i>Drosophila melanogaster</i>	
											Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; <i>Drosophila</i> .	
											1 (bases 1 to 932)	
											Genoscope.	
											Direct Submission	
											Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr ; web : www.genoscope.cns.fr)	
											Determination of this BAC-end sequence was carried out as part of	

Construction of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org/theBDGPdrosophila> melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammos in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPc1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y<sup>1</sup>; cn bw sp, the same strain used for the BDGP's p1 and EST libraries! A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be

Query Match	5.38;	Score 55.6;	DB 12;	Length 932;
Best Local Similarity	30.98;	Pred. No. 0.24;		
Matches 114;	Conservative 80;	Mismatches 175;	Indels 0;	Gaps 0;

[illegible]

RESULT	10	
LOCUS	CNS0091P/C	
DEFINITION	CNS0091P	925 bp DNA
ACCESSION	Drosophila melanogaster genome survey sequence TET3 end of BAC #	linear
VERSION	BA011906 of RPEC-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.	
KEYWORDS	AL053013	
SOURCE	AL053013.1	GI:4934461
ORGANISM	GSS.	
REFERENCE	fruit fly.	
AUTHORS	Drosophila melanogaster	
TITLE	Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
JOURNAL	Pterygota, Neoptera; Endopterygota; Diptera; Brachycera;	
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
	1 (bases 1 to 925)	
	Genoscope.	
	Direct Submission	
	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage	
	Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	
	- web : www.genoscope.cns.fr)	
COMMENT	Determination of this BAC-end sequence was carried out as part of a	

Collaboration of this BAC-end sequence was carried out as part of the Drosophila Genome Project (DGP). The BGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDP Drosophila melanogaster BAC library was prepared by Kazutoyo Oosagawa and Aaron Kammerer in Pletcher de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo.





## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki  
 Toshiyuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMNL at:  
 http://image.llnl.gov  
 Plate: LAM11756 row: a column: 11  
 High quality sequence stop: 687.

## FEATURES

## source

1. 718  
 Location/Qualifiers

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5298706"  
 /clone\_11b="NIH\_MGC\_97"  
 /lab\_host="DH10B"

/note="Organ: testis; Vector: pBluescript (modified  
 pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcag  
 ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTT-3',  
 size selected for average insert size 2.2 kb and  
 normalized to ROP 5. This is a primary library enriched  
 for full-length clones and constructed using the  
 Cap-trapper method (Carninci, in preparation). Library  
 constructed by M. Brownstein (NIH/NHGRI, National  
 Institutes of Health). Note: this is a NIH\_MGC library."

BASE COUNT 119 a 267 c 230 g 102 t

## ORIGIN

Query Match 5.3% Score 55.2; DB 10; Length 718;  
 Best Local Similarity 50.8%; Pred. No. 0.31;

Matches 132; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 349 caccaccacgcgtcattcaccctgagatccggtgtagacagagagacgacta 408  
 Db 66 CACCAACCTGCGAGCTGCGCCCTGGCCCTACAGAACTCTTACGACCCGCGAGTA 125

QY 409 tccacaagaagctgctccgagtgctgctgtagacagagctgtatcgtacagcgag 468  
 Db 126 CCCAGGTACTGCTGAACTCTGACTGCTGCTGCGGGCTGCTACACCGGCTGTCG 185

QY 469 ccgagagacagctgctcaccctgctgctgctgtagacagagctgtgctgtag 528  
 Db 186 CGAGGAGAGAGCTGCGGCTGCGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCG 245

QY 529 ccgagctgctccgagagctgctgtagacagagctgtagacagagctgtgctgtag 588  
 Db 246 CACCCCGGCTGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCG 305

QY 589 cgagttatcaccagctccg 608  
 Db 306 GGGCTGACCTGCTGCTGCG 325

RESULT 13  
 BG809979/c 1137 bp mRNA linear EST 22-MAY-2001  
 LOCUS mgc002xd01f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe

DEFINITION grisea cDNA clone mgc002xd01f 5', mRNA sequence.  
 ACCESSION BG809979  
 VERSION BG809979.1 GI:14180959

KEYWORDS EST.  
 SOURCE Magnaporthe grisea  
 ORGANISM Magnaporthe grisea

REFERENCE 1 (bases 1 to 1137)  
 AUTHORS Choi, W. and Dean, R. A.  
 TITLE Library in the rice blast fungus, Magnaporthe grisea

## JOURNAL

## COMMENT

Unpublished (2001)  
 Contact: Ralph A. Dean  
 Fungal Genomics Laboratory  
 North Carolina State University  
 Campus Box 7251, Raleigh, NC 27695, USA  
 Tel: 919-513-0020  
 Fax: 919-513-0024  
 Email: ralpl@dean.ncsu.edu  
 Seq primer: T3 primer (AATTAACCTTCATTAAGGC).

## FEATURES

## source

1. 1137  
 Location/Qualifiers

/organism="Magnaporthe grisea"  
 /strain="70-15"  
 /db\_xref="taxon:148305"  
 /clone="mgc002xd01f"  
 /clone\_11b="Magnaporthe grisea Appressorium Stage cDNA"  
 /dev\_stage="Germinated conidia on appressorium-inductive  
 surface"

/note="Vector: pBluescript SK(+); Vector; Site\_1: EcoRI;  
 Site\_2: XhoI; The appressorium formation-specific cDNA  
 library was constructed from conidia germinated for 5-8 hr  
 on an inductive surface. The library contains over 55,000  
 clones with average insert size of 1.5 kbp."

## BASE COUNT

67 a 376 c 605 g 14 t 75 others

## ORIGIN

Query Match 5.2% Score 54.8; DB 10; Length 1137;  
 Best Local Similarity 44.7%; Pred. No. 0.38;

Matches 308; Conservative 0; Mismatches 372; Indels 9; Gaps 3;

QY 16 cgtccaaagcagcctccgctccgctccgctccgctccgctccgctccgctccgct 75  
 Db 942 CGCGGGGCG 883

QY 76 tctgacctgctgacacatgctgctgctgctgctgctgctgctgctgctgctgct 135  
 Db 882 GCCCG 823

QY 136 cagtcagctacccacacactgctgctgctgctgctgctgctgctgctgctgctgct 195  
 Db 822 CG 763

QY 196 acacctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 255  
 Db 762 CG 703

QY 256 cctgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 315  
 Db 702 CG 643

QY 316 ggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 370  
 Db 642 CG 583

QY 371 cctgagagatacgtgtgacacagatgagagcgtatccacagaagctgctgctgct 430  
 Db 582 GCG 523

QY 431 gaggctgctgagagagctgctgctgctgctgctgctgctgctgctgctgctgct 490  
 Db 522 CG 464

QY 491 tccgtgagctgctcagagcctgctgctgctgctgctgctgctgctgctgctgctgct 550  
 Db 463 GCG 404

QY 551 tcggagctccacacacctgctgctgctgctgctgctgctgctgctgctgctgct 610  
 Db 403 CG 347

QY 611 ggtgacactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 670

243 QY

[illegible]

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Search completed: September 4, 2002, 01:14:31
Job time: 5029 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 01:52:38 : Search time 16.17 seconds

(without alignments)  
297.578 Million cell updates/sec

Title: US-09-854-280-3

Perfect score: 1073

Sequence: 1 MTLPGILFLTWHTCLAH.....FHTEFLHVPVGCVCVLRV 197

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents-AA:\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*

2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*

3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*

4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*

5: /cgn2\_6/ptodata/2/1aa/6C.COMB.pep.\*

6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	16.1	153	1	US-08-514-014-12
2	173	16.1	153	2	US-08-833-823-12
3	173	16.1	153	3	US-09-034-810-2
4	173	16.1	153	3	US-08-685-239-2
5	160.5	15.0	151	2	US-08-620-694A-8
6	160.5	15.0	151	3	US-09-034-810-6
7	160.5	15.0	151	3	US-09-022-255-8
8	160.5	15.0	151	3	US-09-022-255-8
9	160.5	15.0	151	3	US-08-685-239-6
10	160.5	15.0	151	3	US-09-022-255-8
11	160.5	15.0	151	3	US-09-022-255-8
12	160.5	15.0	151	4	US-09-022-255-8
13	160.5	15.0	151	4	US-09-022-257-8
14	160.5	15.0	151	4	US-08-433-994A-4
15	158	14.7	155	4	US-08-433-994A-8
16	150.5	14.0	158	2	US-08-620-694A-7
17	150.5	14.0	158	3	US-09-022-255-7
18	150.5	14.0	158	3	US-09-022-696-7
19	150.5	14.0	158	3	US-09-022-253-7
20	150.5	14.0	158	3	US-09-022-253-7
21	150.5	14.0	158	4	US-09-022-257-7
22	150.5	14.0	158	4	US-09-022-257-7
23	148.5	13.8	150	3	US-09-034-810-4
24	148.5	13.8	150	3	US-08-685-239-4
25	148.5	13.8	150	4	US-08-433-994A-2
26	148.5	13.8	158	4	US-08-433-994A-10
27	125	11.6	79	4	US-08-433-994A-6

28	83	7.7	430	1	US-08-318-947A-16	Sequence 16, Appl
29	83	7.7	430	2	US-08-795-303-16	Sequence 16, Appl
30	79	7.4	550	1	US-08-318-947A-4	Sequence 4, Appl
31	79	7.4	550	2	US-08-795-303-4	Sequence 4, Appl
32	77.5	7.2	567	1	US-08-261-822A-12	Sequence 12, Appl
33	77.5	7.2	567	5	PCR-US95-07744A-12	Sequence 12, Appl
34	75	7.0	3287	2	US-08-477-451-7	Sequence 7, Appl
35	74.5	6.9	307	2	US-08-918-206-1	Sequence 1, Appl
36	74.5	6.9	555	1	US-08-484-044-6	Sequence 6, Appl
37	74.5	6.9	582	2	US-08-422-659A-9	Sequence 9, Appl
38	74.5	6.9	582	2	US-08-422-706B-9	Sequence 9, Appl
39	74	6.9	260	4	US-09-006-353A-8	Sequence 8, Appl
40	74	6.9	984	2	US-08-449-645A-19	Sequence 19, Appl
41	74	6.9	984	2	US-08-702-367A-19	Sequence 19, Appl
42	74	6.9	984	5	PCR-US95-04681-19	Sequence 19, Appl
43	74	6.9	288	3	US-09-051-019-2	Sequence 2, Appl
44	71.5	6.7	1017	4	US-09-600-776-6	Sequence 6, Appl
45	71	6.6	169	3	US-08-630-172-11	Sequence 11, Appl

## ALIGNMENTS

RESULT 1  
US-08-514-014-12  
Sequence 12, Application US/08514014  
Patent No. 5707829

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

APPLICANT: McCoy, John

APPLICANT: Kelleher, Kerry

APPLICANT: Carlin, McKenough

TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS

TITLE OF INVENTION: ENCODED THEREBY

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESS: Genetics Institute, Inc. -- Legal Affairs

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: USA

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/514,014

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G16000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 153 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-514-014-12

Query Match 16.1%; Score 173; DB 1; Length 153;  
Best Local Similarity 39.0%; Pred. No. 9.4e-13;  
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;  
QY 97 LEADHORSISWRYRVDTDEDRYPQKLAFAACLCRGICIDARTGRTAALNSVRLQSL 156

Db 60 MSRNIESRSTSPWNTYVTWDPNRYSEVVOACRNLGCTINAO-GKEDISMNSVPIQOETL 118  
QY 157 VLRR--PCSRDSSGLPTGAFATHEFTIHPVGTCTVLP 194  
Db 119 VVRRKHQGS-----VSFOLEKVLTVVGTCTVLP 147

## RESULT 2

US-08-833-823-12  
Sequence 12, Application US/08833823  
Patent No. 5969093

GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,823  
FILING DATE: 10-APR-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/514,014  
FILING DATE: 11-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G16000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 876-5851  
TELEFAX: (617) 876-8224

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-833-823-12

Query Match 16.1%, Score 173; DB 2; Length 153;  
Best Local Similarity 39.0%; Pred. No. 9.4e-13;  
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHQSIQSPWRYRVDTEDEYPOKLAFAECLGCGIDARTGRTALNSVRLQSL 156  
Db 60 MSRNIESRSTSPWNTYVTWDPNRYSEVVOACRNLGCTINAO-GKEDISMNSVPIQOETL 118  
QY 157 VLRR--PCSRDSSGLPTGAFATHEFTIHPVGTCTVLP 194  
Db 119 VVRRKHQGS-----VSFOLEKVLTVVGTCTVLP 147

## RESULT 3

US-09-034-810-2  
Sequence 2, Application US/09034810  
Patent No. 6043344  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth

APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debra  
APPLICANT: Mi, Sha  
APPLICANT: Neben, Steven  
APPLICANT: Giannotti, JoAnn  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,810  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,239  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 163 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-034-810-2

Query Match 16.1%, Score 173; DB 3; Length 163;  
Best Local Similarity 39.0%; Pred. No. 1e-12;  
Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

QY 97 LEADTHQSIQSPWRYRVDTEDEYPOKLAFAECLGCGIDARTGRTALNSVRLQSL 156  
Db 70 MSRNIESRSTSPWNTYVTWDPNRYSEVVOACRNLGCTINAO-GKEDISMNSVPIQOETL 128  
QY 157 VLRR--PCSRDSSGLPTGAFATHEFTIHPVGTCTVLP 194  
Db 129 VVRRKHQGS-----VSFOLEKVLTVVGTCTVLP 157

## RESULT 4

US-08-685-239-2  
Sequence 2, Application US/08685239  
Patent No. 6074849  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debra  
APPLICANT: Mi, Sha  
APPLICANT: Neben, Steven  
APPLICANT: Giannotti, JoAnn  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins

NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,239  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-3851  
INFORMATION FOR SEQ ID NO.: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 163 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-685-239-2

Query Match 16.1%; Score 173; DB 3; Length 163;  
Best Local Similarity 39.0%; Pred. No. 1e-12; Indels 14; Gaps 3;  
Matches 39; Conservative 16; Mismatches 31;  
QY 97 LEADTHORSISPMRYVDDEDRYPQKLAFAECLRCGICIDARTGRTALNSVRLQSL 156  
DB 70 MERNIESRSTSPMWTVMTPDRPSEYVQACRNGCINAG-GKEDDISMNSVPIQDEL 128  
QY 157 VLRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCVCVP 194  
DB 129 VVRKHGCS-----VSFOLEKVLVTVGCTCVP 157

RESULT 5  
US-08-620-694A-8  
Sequence 8, Application US/08620694A  
Patent No. 5869286  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, William  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 5869286e1 Receptor That Blinds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694A  
FILING DATE: 21 MARCH 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO.: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-08-620-694A-8

Query Match 15.0%; Score 160.5; DB 2; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;  
QY 36 CYSAEELPLGOAPPHLLAGAKWGALPVALVSSLEAASHRGHHERSATTCQPLVRPE 95  
DB 18 CVKSEITTAQTPRCIAA-----NSFPKSVMTTISIRMMNTSSKRA----- 60  
QY 96 VLEADTHORSISPMRYVDDEDRYPQKLAFAECLRCGICIDARTGRTALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRREDQDRYPSVIMEAKCRILGCVNA-DGVVDVHMNSVPIQDEL 115  
QY 156 VLRR--PCSRDGSGLPTPGAFAFHTEFIHVPVGCVCVP 194  
DB 116 LVVRKHGQCPN-----SFRLEKMLVTVGCTCVP 145

RESULT 6  
US-09-034-810-6  
Sequence 6, Application US/09034810  
Patent No. 6043344  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKenough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debora  
APPLICANT: Mi, Sha  
APPLICANT: Neber, Steven  
APPLICANT: Giannotti, Johann  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/034,810

CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/685,239

ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G12262

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids

TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-034-810-6

Query Match 15.0% Score 160.5; DB 3; Length 151;  
Best Local Similarity 28.6% Pred. No. 2.8e-11;

Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPGQAPPHILARGAKWGQALPVALVSSLEASHGHRHPRPATTCQVLRPEE 95

DB 18 CIVKSEITSAQCPRLAA-----NNSPFSVWVTLSTNNMTSSKRRAS-----60

QY 96 VLEADTHORSTSPWRYRDTDEDRYPOKLARFAECICRCIDARTGRETAALNSVRLQSL 155

DB 61 ----DYNNSTSPWTLHNEQDRPSYIWEAKCRYLGCVA--DGANDYHNSVPIQGEI 115

QY 156 LVLR--RPGSRDGSGLPTPGAFHFTEFIHVPVGCCTVLP 194

DB 116 LVVRKGHPQCPN-----SFRLEKMLVTVGCTCTVTP 145

RESULT 7

US-09-022-255-8

Sequence 8, Application US/09022255

Patent No. 6072033

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

APPLICATION NUMBER: USSN 08/410,535

FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:

NAME: Petkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 587-0430

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 151 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Herpesvirus Saimiri

STRAIN: ORF13

US-09-022-255-8

Query Match

Best Local Similarity 15.0% Score 160.5; DB 3; Length 151;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPGQAPPHILARGAKWGQALPVALVSSLEASHGHRHPRPATTCQVLRPEE 95

DB 18 CIVKSEITSAQCPRLAA-----NNSPFSVWVTLSTNNMTSSKRRAS-----60

QY 96 VLEADTHORSTSPWRYRDTDEDRYPOKLARFAECICRCIDARTGRETAALNSVRLQSL 155

DB 61 ----DYNNSTSPWTLHNEQDRPSYIWEAKCRYLGCVA--DGANDYHNSVPIQGEI 115

QY 156 LVLR--RPGSRDGSGLPTPGAFHFTEFIHVPVGCCTVLP 194

DB 116 LVVRKGHPQCPN-----SFRLEKMLVTVGCTCTVTP 145

RESULT 8

US-09-022-696-8

Sequence 8, Application US/09022696

Patent No. 6072037

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanslow, William

TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,696

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/410,535



FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-696-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHILARGAKWGALPVALVSSLEASHRGRHRRPSATTGCPVLRPE 95  
DB 18 CIVKSEITSAGTPRCIAA-----NNSFPRSVAVTLISIRMMNTSSKRAS----- 60

QY 96 VLEADTHORSISPMRYRYVDDEDYRPOKLAFAECICRGCIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRNEDODRYPSVWEAKCRYLGCVNA-DGVVDYHMNSVPIQGEI 115

QY 156 LVLR--RPCSRRDGSGLTPGAFATHTETIHVPVCTCYLP 194  
DB 116 LVVRKGHQPCHP-----SFRLEKMLVTGCTCTP 145

RESULT 9  
US-08-685-239-6  
Sequence 6, Application US/08685239  
Patent No. 6074849  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: Kelleher, Kerry  
APPLICANT: Carlin, McKeough  
APPLICANT: Goldman, Samuel  
APPLICANT: Pittman, Debra  
APPLICANT: Mi, Sha  
APPLICANT: Neben, Steven  
APPLICANT: Giannotti, JoAnn  
APPLICANT: Golden/Pleet, Margaret  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,239  
FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
REFERENCE/DOCKET NUMBER: G15262  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-685-239-6

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHILARGAKWGALPVALVSSLEASHRGRHRRPSATTGCPVLRPE 95  
DB 18 CIVKSEITSAGTPRCIAA-----NNSFPRSVAVTLISIRMMNTSSKRAS----- 60

QY 96 VLEADTHORSISPMRYRYVDDEDYRPOKLAFAECICRGCIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRNEDODRYPSVWEAKCRYLGCVNA-DGVVDYHMNSVPIQGEI 115

QY 156 LVLR--RPCSRRDGSGLTPGAFATHTETIHVPVCTCYLP 194  
DB 116 LVVRKGHQPCHP-----SFRLEKMLVTGCTCTP 145

RESULT 10  
US-09-022-253-8  
Sequence 8, Application US/09022253  
Patent No. 6096305  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,253  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/620,694  
FILING DATE: 21-MARCH-1996  
APPLICATION NUMBER: USSN 08/538,765  
FILING DATE: 7 AUGUST 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. 6096305 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-253-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

OY 36 CYSAEELPLGQAPPHILARGAKWGALPVALVSSLEASHGRHREPSATTQCPVLRPEE 95  
DB 18 CIVKSEITSAQTPRCILAA-----NSFPRSVAVTILSRNMNTSSKRAS-----60  
OY 96 VLEADTHORSISPMRYRVDTEDRYPOKLAFAECLRCGIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPMTLHRNEDODRPSYIWEAKCRILGCVNA-DGNDVYHMSVPIQOEI 115  
OY 156 LVLR--RPSCRSGSLPFGAFHTEFIHVPVCTCVLP 194  
DB 116 LVVRKGHPCPN-----SFRLEKMLVTVCCTCTVP 145

## RESULT 11

US-09-022-260-8  
Sequence 8, Application US/09022260  
Patent No. 6100235  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,260  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-260-8

Query Match 15.0%; Score 160.5; DB 3; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

OY 36 CYSAEELPLGQAPPHILARGAKWGALPVALVSSLEASHGRHREPSATTQCPVLRPEE 95  
DB 18 CIVKSEITSAQTPRCILAA-----NSFPRSVAVTILSRNMNTSSKRAS-----60  
OY 96 VLEADTHORSISPMRYRVDTEDRYPOKLAFAECLRCGIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPMTLHRNEDODRPSYIWEAKCRILGCVNA-DGNDVYHMSVPIQOEI 115  
OY 156 LVLR--RPSCRSGSLPFGAFHTEFIHVPVCTCVLP 194  
DB 116 LVVRKGHPCPN-----SFRLEKMLVTVCCTCTVP 145

## RESULT 12

US-09-022-259-8  
Sequence 8, Application US/09022259  
Patent No. 6191104  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,259  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-259-8

Query Match 15.0%; Score 160.5; DB 4; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVAVLSLEAASHRGHRRPSATTCQPVLRPEE 95  
DB 18 CIVKSEITSAQTPRCIAA-----NNSFPRSVVTLIRNMNTSSKRAS-----60  
QY 96 VLEADTHOSISPMWRVDTDEDRYPQKLAFAECICRGCIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRREDODRYPVWEAKCRYLGCVNA-DGNVDYHMSVPIQOEI 115  
QY 156 LVLR--RPSRDSGLPTPGAFAFHTFRIHPVGCTCVP 194  
DB 116 LVVRKGHPCPN-----SFRLEKMLTVYGCTCVP 145

RESULT 13  
US-09-022-257-8  
Sequence 8, Application US/09022257  
Patent No. 6197525  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022.257  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620.694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410.535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 151 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Herpesvirus Saimiri  
STRAIN: ORF13  
US-09-022-257-8

Query Match 15.0%; Score 160.5; DB 4; Length 151;  
Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CYSAEELPLGQAPPHLLARGAKWGQALPVAVLSLEAASHRGHRRPSATTCQPVLRPEE 95  
DB 18 CIVKSEITSAQTPRCIAA-----NNSFPRSVVTLIRNMNTSSKRAS-----60  
QY 96 VLEADTHOSISPMWRVDTDEDRYPQKLAFAECICRGCIDARTGRTAALNSVRLQSL 155  
DB 61 ----DYNNSTSPWTLHRREDODRYPVWEAKCRYLGCVNA-DGNVDYHMSVPIQOEI 115  
QY 156 LVLR--RPSRDSGLPTPGAFAFHTFRIHPVGCTCVP 194  
DB 116 LVVRKGHPCPN-----SFRLEKMLTVYGCTCVP 145

RESULT 14  
US-08-432-994A-4  
Sequence 4, Application US/08432994A  
Patent No. 6274711  
GENERAL INFORMATION:  
APPLICANT: Golstein, Pierre  
APPLICANT: Rouvier, Eric  
APPLICANT: Fossiez, Francois  
APPLICANT: Lebecque, Serge J.E.  
APPLICANT: Djossou, Odile  
APPLICANT: Bancheureau, Jacques  
TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/432.994A  
FILING DATE: 02-MAY-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/250.846  
FILING DATE: 27-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/177.747  
FILING DATE: 05-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/077.203

FILING DATE: 14-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0388K3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 151 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-432-994A-4

Query Match 15.0%; Score 160.5; DB 4; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 2.8e-11;  
 Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY 36 CTSAEPLPGQAPPHLLAAGAWGALPVALVSLAASHRGRHPRPSATQCPPLREE 95  
 DB 18 CIVKSEIISAQTPCLIA-----NNSPFRSVWVLTISINWMTSSKRAS----- 60  
 QY 96 VLEADTHOSISPMRYRVDTEDRYPOKLAFAECLRCGCIIDARTGRETALNSVRLQSL 155  
 DB 61 ----DYNRSTSPWNLHREDDRPYSVIMEAKCRHLGCTINA-DGWDVYHNSVPIQDEIIVL 115  
 QY 156 LVLR--RCSRSGSLPTPGAFAFHTEFIHPVGCCTVLP 194  
 DB 116 LVRRKGHPCPN-----SFRLEKMLVTGCTCTVP 145

RESULT 15  
US-08-432-994A-8

Sequence 8, Application US/08432994A

Patent No. 6274711

GENERAL INFORMATION:

APPLICANT: Golstein, Pierre

APPLICANT: Rouvier, Eric

APPLICANT: Fossiez, Francois

APPLICANT: Lebecque, Serge J.E.

APPLICANT: Djossou, Odile

APPLICANT: Banchoireau, Jacques

TITLE OF INVENTION: PURIFIED MAMMALIAN CTLA-8 ANTIGENS AND

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNA Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,994A

FILING DATE: 02-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/250,846

FILING DATE: 27-MAY-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/177,747

FILING DATE: 05-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/077,203

FILING DATE: 14-JUN-1993

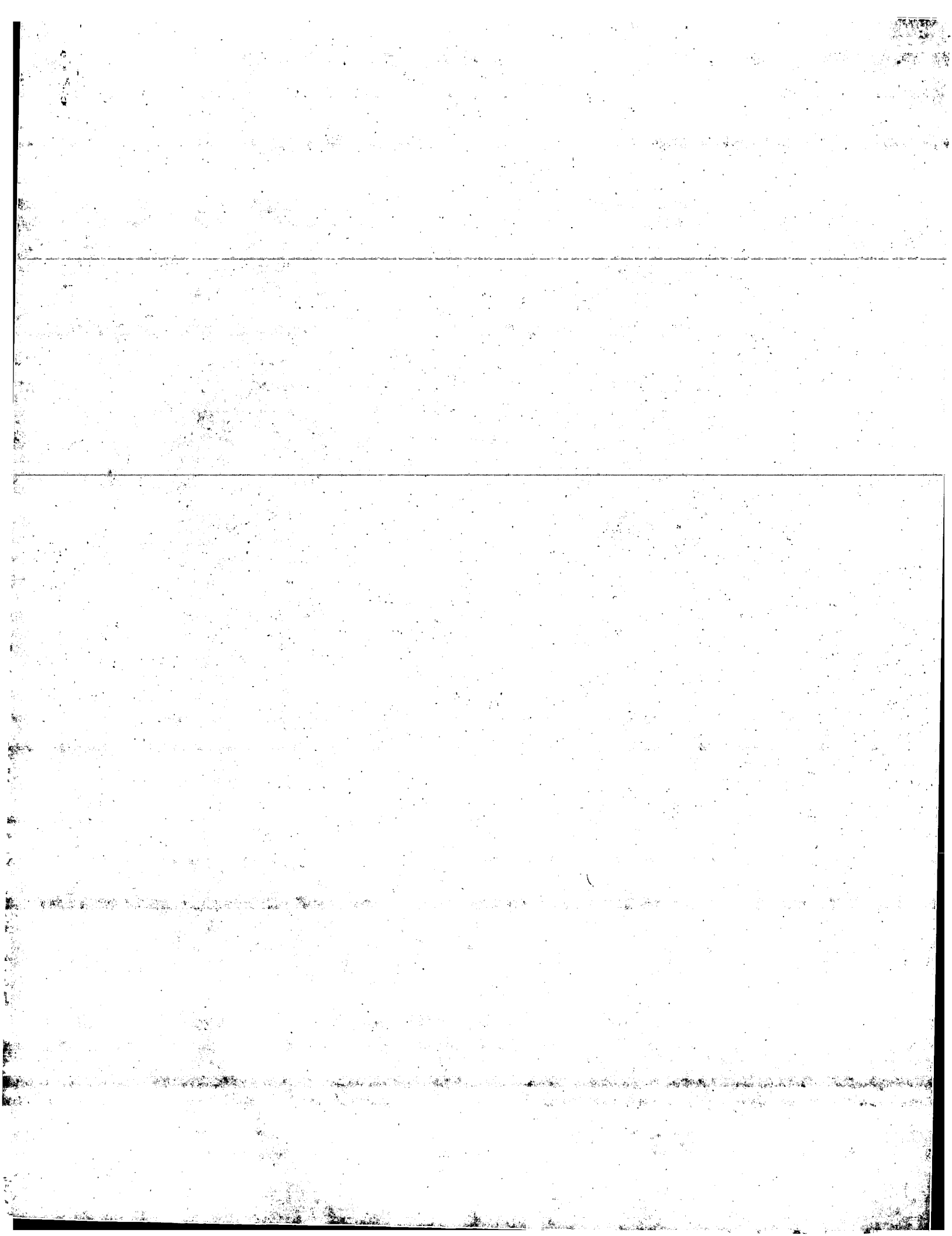
ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 REFERENCE/DOCKET NUMBER: DX0388K3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-9196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 155 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-432-994A-8

Query Match 14.7%; Score 158; DB 4; Length 155;  
 Best Local Similarity 39.8%; Pred. No. 5.7e-11;  
 Matches 39; Conservative 11; Mismatches 34; Indels 14; Gaps 3;

QY 99 ADTHOSISPMRYRVDTEDRYPOKLAFAECLRCGCIIDARTGRETALNSVRLQSL 158  
 DB 64 SDYNRSTSPWNLHREDDRPYSVIMEAKCRHLGCTINA-DGWDVYHNSVPIQDEIIVL 122  
 QY 159 RRRP--CSRSGSLPTPGAFAFHTEFIHPVGCCTVLP 194  
 DB 123 RRRPHPCPN-----SFRLEKILVSGCTCTVP 149

Search completed: September 4, 2002, 01:57:52  
 Job time: 314 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 01:54:03 ; Search time 19.18 Seconds  
(without alignments)  
986.945 Million cell updates/sec

Title: US-09-854-280-3

Perfect score: 1073  
Sequence: 1 MTLPLGLFLFTWLHTCLAH.....FHTFEIHVPVGTCTVLPKRV 197

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160.5	15.0	151	1 BA5351	immediate-early pr
2	148.5	13.8	147	2 JCA628	cytotoxic T-lympho
3	148.5	13.8	150	2 I49623	cytotoxic T-lympho
4	110	10.3	148	2 T21334	hypothetical prote
5	93.5	8.7	395	1 KISM6	galactokinase (EC
6	86.5	8.1	389	2 T50809	hypothetical prote
7	86	8.0	297	2 J10032	hypothetical 31.7K
8	84.5	7.9	1638	2 A42091	transcription acti
9	82.5	7.7	635	2 S76371	hypothetical prote
10	81.5	7.6	325	2 T23218	hypothetical prote
11	81	7.5	553	2 D83640	hypothetical prote
12	80.5	7.5	210	2 B40203	4-alpha-glucanosa
13	80	7.5	411	2 A70509	hypothetical prote
14	79.5	7.4	638	2 UC7753	ring finger B-box
15	79	7.4	549	2 I37386	fas-activated seri
16	79	7.4	887	2 T12514	hypothetical prote
17	79	7.4	885	2 S75894	hypothetical prote
18	78.5	7.3	132	2 E72603	hypothetical prote
19	78	7.3	309	2 T37033	hypothetical prote
20	77.5	7.2	209	2 T30698	hypothetical prote
21	77.5	7.2	323	2 A35909	ira-2 protein - ch
22	77.5	7.2	567	2 E96764	ethylene-insensiti
23	77	7.2	420	2 T14166	fixd protein - Myc
24	77	7.2	466	2 T36212	replication initia
25	77	7.2	639	2 F97670	beta-n-acetylhexos
26	76.5	7.1	639	2 AC2895	beta-N-acetylhexos
27	76.5	7.1	405	2 G84338	3-hydroxy-3-methyl
28	76.5	7.1	503	2 S64787	pre-mRNA splicing
29	76.5	7.1	1882	2 T00069	hypothetical prote

30	76	7.1	296	2 T35477	probable oxidoredu
31	75.5	7.0	1044	2 T00342	hypothetical prote
32	75	7.0	744	2 C75276	sensory box sensor
33	74.5	6.9	464	2 T50955	hypothetical prote
34	74.5	6.9	624	2 B49364	hypothetical prote
35	74	6.9	211	2 G72649	protein kinase (EC
36	74	6.9	260	1 A46517	hypothetical prote
37	74	6.9	347	2 JH0657	CD27 antigen precu
38	73.5	6.8	559	2 S33724	hypothetical 37.5K
39	73.5	6.8	741	2 I48694	transcription fact
40	73	6.8	329	2 T08262	probable transcript
41	73	6.8	373	2 B70673	hypothetical prote
42	73	6.8	1080	2 T43164	probable ddla - My
43	72.5	6.8	181	2 T24914	lacta protein - Li
44	72.5	6.8	362	2 B87571	hypothetical prote
45	72.5	6.8	466	2 A36389	hypothetical prote

## ALIGNMENTS

## RESULT 1

BA5351  
Immediate-early protein 2 - salmirline herpesvirus 1 (strain 11)  
N:Alternate names: hypothetical protein ORF13  
C:Species: salmirline herpesvirus 1  
A:Note: host Salmirl sciurus (common squirrel monkey)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Jul-1999  
C:Accession: BA5351; D36807  
R:Nicholas, J.; Smith, E.P.; Coles, L.; Honess, R.  
Virology 179, 189-200, 1990  
A:Title: Gene expression in cells infected with gammaherpesvirus salmirl: properties  
A:Reference number: A45351; MUID:91021021  
A:Accession: BA5351  
A:Molecule type: mRNA  
A:Residues: 1-151 <NIC>  
A:Cross-references: GB:M60286; NID:9331040; PIDN:AAA46156.1; PID:9331042  
R:Albrecht, J.  
submitted to the EMBL Data Library, January 1992  
A:Description: Primary structure of the herpesvirus salmirl genome..  
A:Reference number: A36806  
A:Accession: D36807  
A:Molecule type: DNA  
A:Residues: 1-151 <ALB>  
A:Cross-references: GB:X64346; NID:960320; PIDN:CAA45636.1; PID:960334  
R:Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; Newman, C.;  
J. Virol. 66, 5047-5058, 1992  
A:Title: Primary structure of the herpesvirus salmirl genome.  
A:Reference number: A37309; MUID:92333688  
A:Contents: annotation: protein-coding frames  
A:Note: neither protein nor nucleotide sequence is given  
C:Genetics:  
A:Gene: 13  
C:Superfamily: salmirl herpesvirus immediate-early protein 2  
C:Keywords: early protein

Query Match: 15.0%; Score 160.5; DB 1; Length 151;  
Best Local Similarity: 28.6%; Pred. No. 1.2e-07;  
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;

QY	36	CYSAEELPLPGAPPHLLAGAKMGQALPVALLVSLEAASHRGHRHSPATTCQPLVRPEE	95
DB	18	CIYKSEITSAQPPCLAA-----NNSFPSSVATLISIRNMWTSKRAS-----	60
QY	96	VLEADTHORSISPMRYRYVDTEDEYPOKLAFCCLRCGICIDARTGRETALNSVRLLOSL	155
DB	61	-----DYNNSTSPWTLHRRDDQDRPSYIWEAKRCVGNV-DGWDVYHNNSSVPIQDEI	115
QY	156	LVLR--RPCSRDGSGLPTPGAFAFHTFEIHVPVGTCTVLP	194
DB	116	LVVRKGHPQCPN-----SFLKMLVYVGTCTVTP	145





Db 303 A---ARRLPRLP-RAGPGRRHGRGLRGP 327

# RESULT 6

hypothetical protein T30N20\_270 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000

C:Accession: T50809

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Men

submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25240

A:Accession: T50809

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-389 <BEV>

A:Cross-references: EMBL:AL365234

A:Experimental source: cultivar Columbia; BAC clone T30N20

C:Genetics:

A:Map position: 5

A>Note: T30N20\_270

Query Match 8.1%; Score 86.5; DB 2; Length 389;  
Best Local Similarity 23.0%; Pred. No. 2.3;  
Matches 56; Conservative 25; Mismatches 83; Indels 79; Gaps 10;

QY 6 GLLFLWHTCLAHNDPSLRGHP---HSHGTPHCYSAEELPLGQAPP-HL-----LA----- 53

Db 44 GVEYLTWSRFTLGSHVNLFLHSQDYNNHSSPLSFSSADLSISAVSFHLNLTNTLAFWKK 103

QY 54 RGAK-----WG-----QALPYALV-----SLEAASHRGHRE 81

Db 104 RGRFSPKIQVWDLSKAKFDSGSEPRSGFTYAVVDDGEMGLLVDSYKEATARKSKAK 163

QY 82 PSATTCPLRPEVLEADTHORSISPMWRYRVTDEDRYPOKLAFACLCRCIDAR--- 138

Db 164 PPTNPQALLRKHEVFGA-----RVFTTKARFGKRRKREISIDCRVEDAKLCE 211

QY 139 -----TGRETAALNSVRLLOSLLV---LRRPCSRDSSGLPTPCAFAP 178

Db 212 SVDSKQVLIKRLMKFRGNEKEVIDGVHVOISMDVYNNLFSKSSGSGGGGGAHVFW 271

QY 179 HTE 181

Db 272 RFE 274

# RESULT 7

hypothetical 31.7K protein (aphe region) - Streptomyces griseus

C:Species: Streptomyces griseus

C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 22-Oct-1999

C:Accession: J10032

R:Heinzel, P.; Weiditzky, O.; Distler, J.; Piepersberg, W.

Arch. Microbiol. 150, 184-192, 1988

A:Title: A second streptomycin resistance gene from Streptomyces griseus codes for strep

A:Reference number: J10031; MUID:86339496

A:Accession: J10032

A:Molecule type: DNA

A:Residues: 1-297 <HEI>

A:Cross-references: GB:M37378; GB:X56876; NID:g153162; PIDN:AAA26701.1; PID:g153164

A:Experimental source: strain N2-3-11

A>Note: the function of the protein is unknown; the orf1 gene and aphe (streptomyces-3"-

C:Genetics:

A:Gene: orf1

C:Superfamily: Streptomyces griseus hypothetical 31.7K protein (aphe region)

Query Match 8.0%; Score 86; DB 2; Length 297;  
Best Local Similarity 27.4%; Pred. No. 1.9;  
Matches 40; Conservative 15; Mismatches 55; Indels 36; Gaps 7;

QY 48 PHLLARGAKWGQALPVAL-----VSSLEASH-----RGHERPSA-----TTO 87

Db 28 PSRLLLG---WNRRAPLVDQLRSTARKSSVEYVADSAVPPGRGEDQPGRGVRFNQ 85

QY 88 CPVLRPEVLEADTHORS-----ISPMWRYRVTDEDRYPOKLAFACLCRCIDARTGRET 143

Db 86 APLSRRETLGLDLDYRDVAVVYLGPDPR-----GCGPDHPDDMTLVALLRLDGRFGRET 141

QY 144 AALNSVRLLOSLLVLRRCSDSG 169

Db 142 -----RVVTELVDDNRRLAPVNSG 161

# RESULT 8

transcription activator SNF2/SWI2 homolog brm - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Sep-1999

C:Accession: A42091

R:Tamkun, J.W.; Deuring, R.; Scott, M.P.; Kissinger, M.; Pattatucci, A.M.; Kaufman, J

Cell 68, 561-572, 1992

A:Title: brhama: a regulator of Drosophila homeotic genes structurally related to the

A:Reference number: A42091; MUID:92154670

A:Accession: A42091

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1638 <TM>

A:Cross-references: GB:M85049; NID:g157011; PIDN:AAA19661.1; PID:g157012

A:Experimental source: Iso-1

A>Note: sequence extracted from NCBI backbone (NCBIN:82354, NCBIIP:82360)

C:Genetics:

A:Gene: FlyBase:brm

A:Cross-references: FlyBase:FBgn0000212

C:Superfamily: unassigned bromodomain proteins; bromodomain homology

C:Keywords: transcription regulation

F.1451-1506/Domain: bromodomain homology <BRO>

Query Match 7.9%; Score 84.5; DB 2; Length 1638;  
Best Local Similarity 22.2%; Pred. No. 17;  
Matches 42; Conservative 26; Mismatches 70; Indels 51; Gaps 8;

QY 22 PSLRGPHSHGPHRCYSAEELPLGQAPP---LLARGAKWGQALPVALVSSLEASHRG 77

Db 52 PCAYGHPRMGRRP-----GCGPRCHMPPRHOGMIFSGKGRMGQMP---PTGRNMSPTQT 104

QY 78 RHRRPSATTQCPYL-----PEVLEADTH---QRSISPMWRYRVTDEDRYPOKLA 125

Db 105 HGMPPNAPTOPCIVSPGCPGPPPPERSSEQLHALORALDSMEKGLQEDPRYSQLLA 164

QY 126 FAELCRGCIIDARTGRETALNSVRLLOS-----LLVLRRCSDSG 166

Db 165 -----MRATSKHQHLNGVNLRLTQITAYRLLRKRPISWMOQALQAQOQPP 215

QY 167 GSGLPYPGA 175

Db 216 GPPIGPPGA 224

# RESULT 9

hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000

C:Accession: S76371

R:Kanehiko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocys

S.

A:Reference number: S74322; MUID:97061201

A:Accession: S76371

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-635 <RAN>  
A:Cross-references: EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BA10223.1; PID:g100159  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: glda protein

Query Match 7.7%; Score 82.5; DB 2; Length 635;  
Best Local Similarity 24.2%; Pred. No. 9.2;  
Matches 44; Conservative 21; Mismatches 60; Indels 57; Gaps 8;

Db 19 HHDSLRGHHSHGTHPCYSAEEL-----PLGAPPHLLARGAKWG--QA 61  
267 HLSPIYGGFIDSKGPRCPSEIDKIVFADKESHQIFIEPEGHDPELYIGFSGTLPEN 326  
QY 62 LPALVSLLEAASHRGHERPSATTCQPVLRPEVEADTHQRSISPMRYVDTEDEDRP 121  
Db 327 VOLAMLOTLPGLN-----CVMLRPAVAYEYDFLPAT-----OCYP 362  
QY 122 QKLA--FAECLRCGICDARTGRETAA-----LNSVRLIQ--SLIVLRRCSDSGSL 170  
Db 363 SLMTKRVAGLEFCAGQINGTGTGEAAAGQVAGINARHCQCKSLIF-----SREGSTL 417  
QY 171 PT 172  
Db 418 GT 419

## RESULT 10

T32218  
hypothetical protein K02B12.1 -Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Feb-2000  
C:Accession: T32218  
R:Harris, B.  
submitted to the EMBL Data Library, July 1996  
A:Reference number: Z19710  
A:Accession: T32218  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-325 <WII>  
A:Cross-references: EMBL:Z75711; PIDN:CA80031.1; GSPDB:GN00019; CESP:K02B12.1  
A:Experimental source: clone K02B12  
C:Genetics:  
A:Gene: CESP:K02B12.1  
A:Map position: 1  
A:Introns: 155/2; 189/3; 234/3; 268/3  
A:Superfamily: transcription factor P1t-1; homeobox homology; POU domain homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 7.6%; Score 81.5; DB 2; Length 325;  
Best Local Similarity 25.9%; Pred. No. 5.5;  
Matches 29; Conservative 14; Mismatches 54; Indels 15; Gaps 4;

QY 9 PLTWLHLCIAHHDPSLRGHPHSHGTHPCYSAEELPLGAPPHLLARGAKWGALPVALYS 68  
Db 12 FQDPHPTMYLQCPQLHFMLEPDMAVPHLAQSLP-----PPHILITS-----TAAVA 59  
QY 69 SLEASHRGHERPSATTCQPVLR-PEVEADTHQRSISPM--RYRVDTE 117  
Db 60 AATIASOSITINOTSVTSPSCQIKQEVERPELIQRLMPMPMPAPVAFQSCDD 111

## RESULT 11

D83640  
hypothetical protein PA0049 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: D83640  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yian, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

..Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A:Reference number: AB2950; MUID:20437337  
A:Accession: D83640

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-553 <STO>  
A:Cross-references: GB:AE00444; GB:AE004091; NID:g9945863; PIDN:AA03439.1; GSPDB:GN  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA0049

Query Match 7.5%; Score 81; DB 2; Length 553;  
Best Local Similarity 24.2%; Pred. No. 11;  
Matches 55; Conservative 16; Mismatches 72; Indels 84; Gaps 13;

QY 12 WLHTCLAHHDPSLRGHHSHGTHPCYSAEELP-----LQAPPHLLARG----- 55  
Db 305 WLEAMNGRFHSSAG--NDGIYCPADSALPNVPLPGSVTPGTAPISLRSGCINP 361  
QY 56 -----AKGQALPVAVSS-----LEASHRGHERPSATTCQPVLRPEVE 98  
Db 362 PRRLGYDASARMQNLPAQFSKASLPVROLADTRGIERPGATSOA-----AEGFD 416  
QY 99 ADTHORSISPMRYRVDTEDEDRYPQKLAFAECLRCGICDARTGRETALNSV--RLQSIL 156  
Db 417 VTWH-----TNDDFPD-----CANRT--ENVPTGNVMMAMPDSL 451

QY 157 VL-----RRRPSRDGSG--LPTGAF-----AFHEF-----IHVY 187  
Db 452 VLPPNRICARNGGQDYLNSESAIVNTVLRDAFRLIEPAGHIVPV 498

## RESULT 12

B40203  
4-alpha-glucanotransferase (EC 2.4.1.25) / amylo-1,6-glucosidase (EC 3.2.1.33) - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 31-Mar-2000  
C:Accession: B40203  
R:Yang, B.Z.; Ding, J.H.; Englund, J.J.; Bao, Y.; Chen, Y.T.  
J. Biol. Chem. 267, 9294-9299, 1992  
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding human muscle glyc  
A:Reference number: AA0203; MUID:92250533  
A:Accession: B40203

A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-210 <YAN>  
A:Superfamily: 4-alpha-glucanotransferase / amylo-1,6-glucosidase  
C:Keywords: glycosidase; glycosyltransferase; hexosyltransferase; hydrolase; polysacc

Query Match 7.5%; Score 80.5; DB 2; Length 210;  
Best Local Similarity 25.3%; Pred. No. 4.2;  
Matches 50; Conservative 17; Mismatches 76; Indels 55; Gaps 10;

QY 22 PSIRGHPHSHGTHPCYS-AEELPIG--QAPPHLLARGAKWGALPVALYSLEASH 75  
Db 3 PTLQKRPVTVTNTPTSCISLADOLELNDPSRPK-----KENMLCITDVVYHNTANS 57  
QY 76 RGRHERPSAT-----TQCPVLRPEEV-----LEADTHQRSISPMRYRVDTEDE 118  
Db 58 RMLHEHPECAYNLVNSPHKALMHLSCDVAEGRGVPALIEDHIMNSI-----RLIITWD 112  
QY 119 RYPOKLAFAECLRCGICDARTGRETALNSVRLQSILVLRRCSDSGSLPTP----- 173  
Db 113 IFPKELLQWGDQVQAVDA-----LPSSTIV--SMACCSGSGTKNNPAAAPS 157  
QY 174 --GAFAHTEFTHVPVC 189  
Db 158 DTGEVNFQSGIIEVPVC 175

RESULT 13  
A:070509  
hypothetical protein RV1230C - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: A70509  
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987  
A:Accession: A70509  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-411 <COL>  
A:Cross-References: GB:298260; GB:AL123456; NID:93261826; PIDN:CAB10927.1; PID:el299939;  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: RV1230C

Query Match 7.5%; Score 80; DB 2; Length 411;  
Best Local Similarity 23.7%; Pred. No. 9.8;  
Matches 45; Conservative 23; Mismatches 78; Indels 44; Gaps 10;  
QY 5 PGLLELTMTLHTCLAHNDPSLRGHPHSHGTP---HCYSAEELPLGQAPPHLLARGAQKQ 60  
DB 85 PPTSFVAVATTSAPPPMIVNSPGALIPAMLSAYRNAELKMAAAP---GCGVSMNL 141  
QY 61 ALPVALVSSLEASHRGHRRPSATQCPVLRP-----BEVLEAD-----TQQRST 106  
DB 142 LAGIGRIESHMA---NGATDARGTAIQPYGPTLDGTLPGNELIIQSSVGNRYTARAM 198  
QY 107 SP-----W-RYRVDTDED-----RYPOKIAFAECICRGCIDARTGRET-AAL----- 146  
DB 199 GPMQFLPGWVARYATDGGDDGVADPQNLFDSTLAARLYCSCGLNLRDPAQVAAALLRYN 258  
QY 147 NSVRLQSL 156  
DB 259 NSMPYAQNV 268  
RESULT 14  
JC7753  
ring finger B-box coiled-coil protein, GOA - human  
C:Species: Homo sapiens (man)  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 14-Dec-2001  
C:Accession: JC7753  
R:Yandepulte, D.A.A.; Meije, C.B.; van Driel, M.; Leenstra, S.; IJlst-Lelz, H.; Das, Biochem. Biophys. Res. Commun. 286, 574-579, 2001  
A:Title: GOA, a novel gene encoding a ring finger B-box coiled-coil protein, is overexpressed  
A:Reference number: JC7753; MUID:21402356; PMID:11511098  
A:Accession: JC7753  
A:Molecule type: DNA  
A:Residues: 1-638 <VAN>  
A:Cross-References: GB:AY026763  
C:Comment: This protein, a member of the subfamily of the ring finger proteins, has an as well.  
C:Genetics:  
A:Gene: goa  
A:Map position: 17q24-25

Query Match 7.4%; Score 79.5; DB 2; Length 638;  
Best Local Similarity 30.3%; Pred. No. 18;  
Matches 36; Conservative 10; Mismatches 56; Indels 17; Gaps 6;  
QY 40 EELPLGQAPPHLLARGAQKQALPVAL--VSSLEA--ASHRGHRRPSATQCPVLRPEE 95  
DB 118 EPWPAGEEP--VRDACPCEGALPALSCISCLASFCPAHLGPHRRSPALRGHRLVPLR 175

QY 96 VLEADTHORSISPMRYRVDTDEDYPOKIAFAECICRG-CIDARTGRETALNSVLLQ 153  
DB 176 RLEESICPHRLRL-----ERYCR--AERYCCECAQAEHREHLEVPLEQERALQ 224

RESULT 15  
I37386  
fas-activated serine/threonine kinase - human  
C:Species: Homo sapiens (man)  
C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 21-Jul-2000  
C:Accession: I37386  
R:Tian, Q.; Taupin, J.; Ellgedge, S.; Robertson, M.; Anderson, P. J. Exp. Med. 182, 865-874, 1995  
A:Title: Fas-activated serine/threonine kinase (FAST) phosphorylates TIA-1 during Fas  
A:Reference number: I37386; MUID:95378805  
A:Accession: I37386  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-549 <RES>  
A:Cross-References: EMBL:X86779; NID:q1006658; PIDN:CAA60448.1; PID:q1006659  
C:Genetics:  
A:Gene: fast  
C:Superfamily: human fas-activated serine/threonine kinase

Query Match 7.4%; Score 79; DB 2; Length 549;  
Best Local Similarity 28.6%; Pred. No. 17;  
Matches 56; Conservative 12; Mismatches 58; Indels 70; Gaps 12;  
QY 13 LHTCLAHNDPSLRGHPHSHGTPHCYSAEE--LPGLGAPPHLLARGAQKQALPVA----- 65  
DB 158 IHVCL--HLAVLGLFP--SDGPLVCALEQERRRLRPKPPPLQPLLRGGQLEALSCSR 214  
QY 66 -----LVSSL-EE-----ASHRGHRRPSATQCPVLRPEVLEADTH- 102  
DB 215 FLRYPQHILSLAEARPEELPHVAVLLAQHLARRH-----LREPOLLEAIHF 264  
QY 103 -----QRSISF---RYRVDTDEDYPOKIAFAECICRGCIDARTGRETAL 146  
DB 265 LVVQETQLSSKVVQKLVLPGRILN-----LPLEQGMPLER--ILAKRA-GVADP 313  
QY 147 NSVRLQSLVLRRP 162  
DB 314 ATVNILMSLCQLRCLP 329

Search completed: September 4, 2002, 01:58:34  
Job time: 271 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 01:56:43 ; Search time 10.9 seconds  
(without alignments)  
699.794 Million cell updates/sec

Title: US-09-854-280-3

Perfect score: 1073  
Sequence: 1 MTLPLGLLFTWLHTCLAHH.....FHTTEFIHVPGCTCVLPRSV 197

Scoring table: BIOSIM62  
Gapop-10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	117C_HUMAN	O9P0M4 homo sapien
2	173	10.1	153	117F_HUMAN	O9P0M4 homo sapien
3	168.5	15.7	180	117B_MOUSE	O9P0M4 mus musculu
4	165.5	15.4	177	117E_HUMAN	O9P0M4 homo sapien
5	160.5	15.0	151	VG13_HSVSA	P24916 herpesvirus
6	158	14.7	155	1117_HUMAN	O16552 homo sapien
7	157.5	14.7	151	VG13_HSVSC	O40833 herpesvirus
8	157.5	14.7	178	117B_MESAU	O9P0M4 mesocricetu
9	154.5	14.4	180	117B_HUMAN	O9P0M4 homo sapien
10	148.5	13.8	150	1117_RAT	O61453 rattus norv
11	148.5	13.8	158	1117_MOUSE	O61453 mus musculu
12	85.5	8.0	465	HNF6_HUMAN	O9P0M4 homo sapien
13	85.5	8.0	465	HNF6_MOUSE	O08755 mus musculu
14	85.5	8.0	465	HNF6_RAT	P70512 rattus norv
15	84.5	7.9	1638	BRM_DROME	P25439 drosophila
16	82.5	7.7	635	GIDA_SYNY3	O55694 synecocyst
17	81.5	7.6	325	HM06_CAEEL	P20068 caenorhabdi
18	79	7.4	549	FAST_HUMAN	O14296 homo sapien
19	77.5	7.2	323	FR42_CHICK	P18625 gallus galli
20	77.5	7.2	581	TR14_HUMAN	O15650 homo sapien
21	76.5	7.1	503	PR19_YEAST	O09013 homo sapien
22	74.5	6.9	639	DMK_HUMAN	P26842 homo sapien
23	74	6.9	260	TNR7_HUMAN	P21709 homo sapien
24	74	6.9	976	EPAL_HUMAN	P70478 rattus norv
25	74	6.9	2842	ARC_RAT	O03365 sus scrofa
26	73.5	6.8	559	HNF6_PIG	O61985 mus musculu
27	73.5	6.8	741	NFL1_MOUSE	P95114 mycobacteri
28	73	6.8	373	DDL_MYCTU	P23824 gallus galli
29	72.5	6.8	466	GAT2_CHICK	P79761 gallus galli
30	72.5	6.8	528	CP15_CHICK	O14494 h nuclear f
31	72.5	6.8	772	NFL1_HUMAN	P52086 escherichia
32	71.5	6.7	203	COBC_ECOLI	O9myv3 canis famli
33	71.5	6.7	214	VEGA_CANFA	

34	71.5	6.7	297	1	HXAB_CHICK	P31258 gallus galli
35	71.5	6.7	433	1	PMER_ERMCH	O47474 erwina chr
36	71	6.6	322	1	POS_AVINC	P23050 avian retro
37	71	6.6	342	1	CRIB_STRGR	P54977 streptomyc
38	71	6.6	367	1	FOS_CHICK	P11939 gallus galli
39	71	6.6	2564	1	SPCQ_HUMAN	O9h254 homo sapien
40	70.5	6.6	256	1	KPYA_AERPE	O9yfp5 aeropyrum p
41	70.5	6.6	313	1	HXAB_MOUSE	P31311 mus musculu
42	70.5	6.6	705	1	PIXB_MOUSE	O9es28 mus musculu
43	70	6.5	381	1	SELP_MOUSE	P48908 homo sapien
44	70	6.5	411	1	HOX3_BRATL	P50901 branchiosto
45	70	6.5	839	1	ZF95_HUMAN	O9y218 homo sapien

## ALIGNMENTS

```

RESULT 1
ID 117C_HUMAN STANDARD: PRT; 197 AA.
AC O9P0M4: O9HC75:
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-17C precursor (IL-17C) (Cytokine CX2).
GN IL17C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20105548; PubMed=10639155;
RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,
RA Gurney A.L., Wood W.L.;
RT "Cloning and characterization of IL-17B and IL-17C, two new members
RT of the IL-17 cytokine family."
RL Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhang W., He L., Wan T., Yuan Z., Gao X.;
RT "Novel human cytokine CX2 with homology to IL-17."
RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
CC - FUNCTION: Stimulates the release of tumor necrosis factor alpha
CC and IL-1beta from the monocytic cell line THP-1.
CC - SUBCELLULAR LOCATION: Secreted.
CC - SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC -----
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CC -----
DR EMBL: AF152099; AAF28105.1; -
DR EMBL: AF142410; AAG27921.1; -
DR MIM: 604628; -
KW Cytokine; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 197 INTERLEUKIN-17C.
FT DISULFID 129 189 BY SIMILARITY.
FT DISULFID 134 191 BY SIMILARITY.
FT CONFLICT 50 50 H -> R (IN REF. 2).
SQ SEQUENCE 197 AA; 21765 MW; BAE0152E18DE7D08 CRC64;
Query Match 100.0%; Score 1073; DB 1; Length 197;
Best Local Similarity 100.0%; Pred. No. 5.4e-94;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MTLPLGLLFTWLHTCLAHHPSLRNGHPHSHGTPHCYSAEELPLGQAPPHLARGAKWQ 60

```



RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldi M.F.,  
 RA Brownstein M.J., Bult C., Fletcher P., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RA \*Functional annotation of a full-length mouse cDNA collection.\*;  
 RA Nature 409:685-690(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RL Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha  
 CC and IL-1beta from the monocytic cell line THP-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
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 CC -----  
 DR EMBL: AF184970; AAF01319.1; -  
 DR EMBL: AF218726; AAC44135.1; -  
 DR EMBL: AF250308; AAK37427.1; -  
 DR EMBL: AK003506; BAB22826.1; -  
 DR EMBL: BC002271; AAH02271.1; -  
 DR MGI: 1928397; I117b.  
 KW Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 180  
 FT DISULFID 121 176  
 FT DISULFID 126 178  
 FT CARBOHYD 75 75  
 FT CONFLICT 1 33  
 FT CONFLICT 34 34  
 FT CONFLICT 65 65  
 FT CONFLICT 76 76  
 FT SEQUENCE 180 AA; 20309 MW; E26F4C72001997C5 CRC64;  
 Query Match 15.7%; Score 168.5; DB 1; Length 180;  
 Best Local Similarity 27.0%; Pred. No. 5.5e-09;  
 Matches 53; Conservative 28; Mismatches 82; Indels 33; Gaps 6;

QY 7 LLELTLMTHTCLA-HHDBSLRGHSHGTPHCYSABELPLGQAPPHLLARAKMGQALPVA 65  
 DB 7 LLELTLMTHTCLA-HHDBSLRGHSHGTPHCYSABELPLGQAPPHLLARAKMGQALPVA 65  
 QY 66 LVSLEASHRGHRRSPATTCPLVLRPEVLEAD-----THORSISPMRYRDTD 116  
 DB 66 LVSLEASHRGHRRSPATTCPLVLRPEVLEAD-----THORSISPMRYRDTD 116  
 QY 49 LVSRYVRYAMEYERLGMVAQDLNRSSSPAKKCEVNIQMLSNKRSISPFGYSINHD 108  
 DB 49 LVSRYVRYAMEYERLGMVAQDLNRSSSPAKKCEVNIQMLSNKRSISPFGYSINHD 108  
 QY 117 EDRYPKLAFAECLRCGIDARTGRETALNSVRLQSLVLRPPSRDGSGLPTPGAP 176  
 DB 117 EDRYPKLAFAECLRCGIDARTGRETALNSVRLQSLVLRPPSRDGSGLPTPGAP 176  
 QY 109 PSRIPADLPARCLICGVNPFMTQEDBSKSVYVVF-SGVVRRRLCPGP-----PRGPGC 163  
 DB 109 PSRIPADLPARCLICGVNPFMTQEDBSKSVYVVF-SGVVRRRLCPGP-----PRGPGC 163  
 QY 177 AFHTERFHVVGCTCV 192  
 DB 177 AFHTERFHVVGCTCV 192  
 QY 164 RQRYMETTAVGCTCI 179  
 DB 164 RQRYMETTAVGCTCI 179

RESULT 4  
 ID 117E.HUMAN STANDARD; PRT; 177 AA.  
 AC 09H293;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 GN Interleukin-17E precursor (IL-17E).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21125711; PubMed=11058597;  
 RA Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,  
 RA Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;  
 RT IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog  
 RT IL-17Rb1.\*;  
 RL J. Biol. Chem. 276:1660-1664(2001)  
 CC -1- FUNCTION: Induces activation of NF-kappaB and stimulates  
 CC production of the proinflammatory chemokine IL-8.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed at low levels in several tissues,  
 CC including brain, kidney, lung, prostate, testis, spinal cord,  
 CC adrenal gland, and trachea.  
 CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
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 CC -----  
 DR EMBL: AF305200; AAG40848.1; -  
 DR MIM: 605658; -  
 KW Cytokine; Glycoprotein; Signal.  
 FT SIGNAL 1 32  
 FT CHAIN 33 177  
 FT DISULFID 110 168  
 FT DISULFID 115 170  
 FT CARBOHYD 136 136  
 FT SEQUENCE 177 AA; 20330 MW; 52D895710CD59871 CRC64;  
 Query Match 15.4%; Score 165.5; DB 1; Length 177;  
 Best Local Similarity 29.7%; Pred. No. 1e-08;  
 Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;

QY 27 HPHSHGTPHCYS-----AEELPLGQAPPHLLARAKMGQALPVYSSLEASHRGHRR 81  
 DB 31 HTYSHWSPSCPCSGQDPTSEL-----LRW-STVP---VPLPAPRRHPPS 73  
 QY 82 PSATTCQPLVLRPEVLEADTHORSISPMRYRDTDERYRQKLAFAECLRCGIDARTG 141  
 DB 74 CRASEDQPL-----NSRAISPMRYELDRDLRLPQDLYHARCLCPHCVSLOTGS 122  
 QY 142 EATAAL-NSVRLQSLVLRPPSRDGSGLPTPGAFHFHEFHVVGCTCVPR 195  
 DB 123 HMDPRGNSELLYNQVYFYRRPCHGEG---TIKGCLERLRYSLACVCPRR 174  
 RESULT 5  
 ID VG13.HSVSA STANDARD; PRT; 151 AA.  
 AC P24916;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)

```

Query Match      15.0%; Score 160.5; DB 1; Length 151;
Best Local Similarity 28.6%; Pred. No. 2.6e-08;
Matches 46; Conservative 23; Mismatches 57; Indels 35; Gaps 5;
07 36 CYSAEELPLGAPPHLLARGAKWGQALPVALVSSLEAASHRGRIERSATQCPVLRPEE 95

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Qy	96	VLEADTHORISIPRRVYDDEDYDQYPOKLF	AECIGCIDARGRETAALNSYRLOS	155
Db	61	-----DYNRSSSPPTLHRNEDQDQRP	SVIWEAKORYGCVNA-DGNVDYHMNSVPIQOET	115
Qy	156	LYLRR--RPGSRDGGSLPTPOAF	AFHTEFLHVPVGCTVLP	194
Db	116	LYVRKHQPCPN-----SFLRLEKMLVVGCTVLP		145

RESULT	6
IL17	HUMAN
ID	IL17_HUMAN
AC	016552;
DT	01-NOV-1997 (Rel. 35, Created)
DR	01-NOV-1997 (Rel. 35, Last sequence update)
DT	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Interleukin-17 precursor (IL-17) (IL-17A) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).
GN	IL17 OR IL17A OR CTLA8.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NC	NCBI_Taxid:9606;
RP	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE-96281911; PubMed-8676080.
RA	Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Alt-Yahia S.,
RA	Mat C., Pln J.-U., Garrone P., Garcia E., Sealand S., Blanchard D.,
RA	Gaillard C., Das Mahapatra B., Rouvier E., Golstein P., Banchereau J.,
RA	Lebecque S.;
RT	"T cell interleukin-17 induces stromal cells to produce
RT	proinflammatory and hematopoietic cytokines."
RL	J. Exp. Med. 183:2593-2603(1996).
RP	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE-T-cell;
RX	MEDLINE-96094436; PubMed-7499828;
RA	Yao Z., Palnter S.L., Fanslow W.C., Ulrich D., Macduff B.M.,
RA	Spriggs M.K., Armitage R.J.;
RT	"Human IL-17: a novel cytokine derived from T cells."
RL	J. Immunol. 155:3483-3486(1995).
CC	- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND
CC	HEMATOPOIETIC CYTOKINES. ENHANCES THE SURFACE EXPRESSION OF THE
CC	INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN FIBROBLASTS.
CC	- SUBUNIT: HOMODIMER.
CC	- TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS.
CC	- PTM: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS.
CC	- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC	- DATABASE: NAME=Ref Systems/ cytokine mini-reviews: il17;
CC	WWW="http://www.indsystems.com/asp/q.steibullder.asp?bodyId=211"
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL, Z58820; CAA91233.1; -
DR	EMBL, U32659; AAC50341.1; -
DR	MIM, 603149; -
KW	Cytokine; Glycoprotein; T-cell; Antigen; Signal.
FT	SIGNAL 1 23
FT	CHAIN 155
FT	DISULFID 24 155
FT	DISULFID 94 144
FT	DISULFID 99 146
FT	CARBOHYD 68 68
FT	SEQUENCE 155 AA; 17504 MW; ZBCA9CB2F4886D1 CRC64; (POTENTIAL).

	Query Match	14.7%	Score 158;	DB 1;	Length 155;
	Best Local Similarity	39.8%;	Pred. No.	4.5e-08;	
	Matches	39;	Conservative	11;	Mismatches 34; Indels 14; Gaps 3;
OY	ADTQRSISPRWRYVDDEDEDPKIAFAETLGCSCIDARTGRTALNVRLOSLIVL	158.			
	: :         :	:       :	:	:	
Dd	SDYYRSTSPWNLRHNDPERPYSVIEAKCRHGICLN-DGNANDYMNSVPIDQETLV	122			
OY	RRRP--CSRDSGLPTPGAFATHTFTTHVGCTCVAL	194			



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DB 123 RREPCHPN-----SFRLEKILVSGCTCVP 149

RESULT 7
VG13_HSVSC STANDARD: PRT: 151 AA.
AC 040633;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE Immediate early gene 13 protein precursor.
OS Herpesvirus saimiri (subgroup C / strain 488).
OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10384;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98037620; PubMed=9371569;
RA Knappe A., Hiller C., Thurn M., Wiltmann S., Hofmann H.,
RA Fleckenstein B., Fieckenscher H.;
RT "The superantigen-homologous viral immediate-early gene iel4/vsag in
RT herpesvirus saimiri-transformed human T cells.";
RL J. Virol. 71:9124-9133(1997).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC -----
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CC -----
DR EMBL: Y13183; CAA73627.1;
KW Cytokine; Early protein; Signal.
FT CHAIN 1 22
FT SIGNAL 1 22
FT DISULFID 23 151
FT DISULFID 90 140
FT DISULFID 95 142
FT CARBOHYD 36 36
FT CARBOHYD 53 53
FT CARBOHYD 64 64
FT SEQUENCE 151 AA: 17189 MW: 49829430C46BE32 CRC64;

Query Match 14.7%; Score 157.5; DB 1; Length 151;
Best Local Similarity 28.6%; Pred. No. 4.9e-08;
Matches 46; Conservative 22; Mismatches 58; Indels 35; Gaps 5;

OY 36 CTSAEELPLPGQAPPHLLANGAKMGQALPVALLYSLEASHRGHRRPSATTQCPVLRPEE 95
DB 18 CIVKSTSTSAQTPRCIAA-----NNSFPRSVVLTLSIRNMWTSKRA----- 60

OY 96 VLEADTHOSISPMRYRVDTDEDRYPQKLAFAECLRCGICDARTGRTALNSVRLQSL 155
DB 61 ----DYNSTSPWLYRNEDDRIPTVWEAKCRYLGVNA-DGNVDYHMSVPIQDEI 115

OY 156 LVLR--RPSRDGSGLPTPGAFATHTFEIHPVGCCTVP 194
DB 116 LVVRKCHNCPN-----SFRLEKMLVTVGCTCVP 145

RESULT 8
I17B_MESAU STANDARD: PRT: 178 AA.
AC 09E016;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-17 precursor (IL-17B) (Neuronal Interleukin-17 related
DE factor) (Fragment).

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GN IL17B OR N1RF.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RA Moore E.E., Presnell S., Garrigue U., Guilhot A., LeGuern E.,
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuester R.E.;
RT "Identification of a novel IL-17 related factor: demonstration of
RT neuronal expression and evaluation as a candidate for the chromosome
RT 5q-linked form of Charcot-Marie-Tooth disease.";
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Stimulates the release of tumor necrosis factor alpha
CC and IL-1beta from the monocytic cell line THP-1 (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.
CC -----
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CC -----
DR EMBL: AF218725; AAG4134.1;
KW Cytokine; Glycoprotein; Signal.
FT CHAIN 1 22
FT SIGNAL 1 22
FT DISULFID 23 >178
FT CARBOHYD 75 75
FT DISULFID 121 176
FT DISULFID 126 178
FT NON_TER 178
FT SEQUENCE 178 AA: 20071 MW: 03D02D60BEC9A51 CRC64;

Query Match 14.7%; Score 157.5; DB 1; Length 178;
Best Local Similarity 29.5%; Pred. No. 5.9e-08;
Matches 46; Conservative 23; Mismatches 70; Indels 17; Gaps 4;

OY 45 GOAPPLRLGAKMGQALPVALLYSLEASHRGHRRPSATTQCPVLRPEVLEAD----- 100
DB 31 GOVREPPLAPGP---HOVLVLVSRYKPYARKMEYERNLGENVAQLRNSSEPAKRCCEVN 87

OY 101 ----THORSISPMRYRVDTDEDRYPQKLAFAECLRCGICDARTGRTALNSVRLQSL 155
DB 88 LQWLMSNKRSLSPWGISINHDPRIADLPPEARCLICGVNPPTMQEDRSVSVPF-SQ 146

OY 156 LVLR--RPSRDGSGLPTPGAFATHTFEIHPVGCCTC 191
DB 147 VEVRRRLCPPP-----PRGPCRHRYVETJAVGCTC 178

RESULT 9
I17B_HUMAN STANDARD: PRT: 180 AA.
AC 09DHF5;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Interleukin-17 precursor (IL-17B) (Cytokine-like protein ZCYT07)
DE (Neuronal Interleukin-17 related factor) (Interleukin-20).
GN IL17B OR ZCYT07 OR N1RF OR IL20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;

```

Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
[2]  
SEQUENCE FROM N.A.  
RA MEDLINE-60317118; PubMed-10749887;  
RA Shi Y., Dillisch S.J., Zhang J., Connolly K., Grzegorzewski K.J.,  
RA Barber M.C., Wang W., Mathen K., Fisher C.L., Olsen H.,  
RA Riden S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,  
RA Carrell J.A., Ebner R.,  
RT "A novel cytokine receptor-ligand pair. Identification, molecular  
RT characterization, and in vivo immunomodulatory activity."  
RL J. Biol. Chem. 275:19167-19176(2000).  
RN [3]  
SEQUENCE FROM N.A.  
RA MEDLINE-2010548; PubMed-10639155;  
RA Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,  
RA Gurney A.L., Wood W.I.,  
RT "Cloning and characterization of IL-17B and IL-17C, two new members  
RT of the IL-17 cytokine family." 97:773-778(2000).  
RN [4]  
Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).  
RA SEQUENCE FROM N.A.  
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., Leguenn E.,  
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kresner R.E.,  
RT "Identification of a novel IL-17 related factor: demonstration of  
RT neuronal expression and evaluation as a candidate for the chromosome  
RT 5q-linked form of Charcot-Marie-Tooth disease." 97:773-778(2000).  
RN [5]  
Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RA SEQUENCE FROM N.A.  
RA Zhang W., Wang J., Cao X.,  
RT "Novel cytokine homology with interleukin-17."  
RT Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [6]  
SEQUENCE FROM N.A.  
RA Rieder M., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nickerson D.A.,  
RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [7]  
FUNCTION: Stimulates the release of tumor necrosis factor alpha  
CC and IL-beta from the monocytic cell line THP-1.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed in adult pancreas, small intestine,  
CC stomach, spinal cord and testis. Less pronounced expression in  
CC prostate, colon mucosal lining, and ovary.  
CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
CC  
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CC  
DR EMBL: AF184969; AAF01318.1;  
DR EMBL: AF212311; AAF78775.1;  
DR EMBL: AF152098; AAF28104.1;  
DR EMBL: AF218727; AAG4136.1;  
DR EMBL: AF110385; AAG39637.1;  
DR EMBL: AF386077; AAK60336.1;  
DR MIM: 604627;  
KM Cytokine; Glycoprotein; Signal.  
FT CHAIN 1 20  
FT SIGNAL 1 20  
FT CHAIN 21 180  
FT DISULFID 121 176  
FT DISULFID 126 178  
FT CARBOHYD 75 75  
FT SEQUENCE 180 AA; 20437 MW; F1B0BC1446D0B14A CRC64;  
Query Match 14.4%; Score 154.5; DB 1; Length 180;  
Best Local Similarity 28.7%; Pred. No. 1,1e-07;  
Matches 45; Conservative 25; Mismatches 70; Indels 17; Gaps 4;

OY 45 GQAPHLARGAKMGQALPVVALVSSLEASHRGHERSATTOCPVLRPEVLEAD---- 100  
DB 31 GQGRGPIAPGP---HQVPLDVSBMKRYAMEERIEEMVAQLNSSELRQKCEVN 87  
OY 101 -----THQSTSPMYRYVDDEDRYPOKLAFAECICRGCIDARTGRTAALNSVRLQSL 155  
DB 88 LQWMSNRSLSPMGYSINHPDSRIPLDLPPEARCLGCVNPFIMQDRSMVSPVF-SQ 146  
OY 156 LVLRPPCSRRSGSLPFGAFAFEFEIHPVGCTCV 192  
DB 147 VPRRRICPPP-----PRGPCORAVMETTAVGCTCI 179  
RESULT 10  
IL17-RAT STANDARD: PRT: 150 AA.  
AC 061453;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated  
DE antigen 8) (CTLA-8).  
GN IL17 OR CTLA8.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RA SEQUENCE FROM N.A.  
RA MEDLINE-93294300; PubMed-8390535;  
RA Rouvier E., Luciani M.F., Mattei M.-G., Denizot F., Golstein P.,  
RT "CTLA-8, cloned from an activated T cell, bearing an AU-rich messenger  
RT RNA instability sequences, and homologous to a herpesvirus salm1r1  
RT gene." 150:5445-5456(1993).  
RN [2]  
RN J. Immunol. 150:5445-5456(1993).  
RN ORGANISM IDENTIFICATION.  
RA MEDLINE-96194901; PubMed-8654948;  
RA Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.,  
RT "Complete nucleotide sequence of the mouse CTLA8 gene." 166:223-225(1996).  
RN [3]  
RA SEQUENCE FROM N.A. AND ORGANISM IDENTIFICATION.  
RA MEDLINE-97031826; PubMed-8877732;  
RA Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A.,  
RA Wagner J.L., Hannum C.H., Zlotnik A.,  
RT "Mouse IL-17: a cytokine preferentially expressed by alpha beta TCR +  
RT CD4-CD8-T cells." 16:611-617(1996).  
RN J. Interferon Cytokine Res. 16:611-617(1996).  
CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND  
CC HEMATOPOIETIC CYTOKINES (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER. (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE FROM MOUSE BUT, ON  
CC THE BASIS OF SUBSEQUENT WORK (REF.2 AND REF.3), HAS BEEN SHOWN TO  
CC BE OF RAT ORIGIN.  
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CC  
DR EMBL: L13839; AAA37490.1;  
KM Cytokine; Glycoprotein; T-cell; Antigen; Signal.  
FT CHAIN 1 17  
FT SIGNAL 1 17  
FT CHAIN 18 150  
FT DISULFID 89 139  
FT DISULFID 94 141  
FT CARBOHYD 63 63  
FT SEQUENCE 150 AA; 16337 MW; F1B0BC1446D0B14A CRC64;  
Query Match 14.4%; Score 154.5; DB 1; Length 180;  
Best Local Similarity 28.7%; Pred. No. 1,1e-07;  
Matches 45; Conservative 25; Mismatches 70; Indels 17; Gaps 4;

FT CONFLICT 46 46 I -> L (IN REF. 3).  
SQ SEQUENCE 150 AA: 16876 MW: EF13F33EDF9D689F CRC64;

Query Match 13.8%; Score 148.5; DB 1; Length 150;  
Best Local Similarity 29.4%; Pred. No. 3.4e-07;  
Matches 45; Conservative 20; Mismatches 55; Indels 33; Gaps 5;

OY 42 LPLGAPPLILRGAKMGQALPVALYSSLEASHGRHSPSATTTQCPLYRREVELEADT 101  
DB 21 IQSSVCPAEANFNLFONKVKLVKINSLSKASSRRPS-----DY 61  
OY 102 HORSISPMWRVYDTEDEDRYPQKLAFAECRCICIDARTGRETAALNSVLLQSLYLRRR 161  
DB 62 LNRSTSPMTLSRNEDEPDRPSYIWEAQCRHRCVNAE-GKLDHNNNSVLIQOEIILVKRE 120  
OY 162 P--CSRDGSGLPFGAFHFEFIHVPVGCCTV 192  
DB 121 PEKCG-----PFTFVEKMLVGVCCTCV 142

RESULT 11  
IL17\_MOUSE STANDARD: PRT; 158 AA.

AC Q62386; Q60971;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Interleukin-17 precursor (IL-17) (Cytotoxic T lymphocyte-associated antigen 8) (CTLA-8).  
GN IL17 OR CTLA8.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C; TISSUE=Thymocytes;  
RX MEDLINE=97031826; PubMed=8877732;  
RA Kennedy J., Rossi D.L., Zurawski S.M., Vega F. Jr., Kastelein R.A., Wagner J.L., Hannum C.H., Zlotnik A.;  
RT "Mouse IL-17: a cytokine preferentially expressed by alpha beta TCR + CD4-CD8-T cells.";  
RL J. Interferon Cytokine Res. 16:611-617(1996).  
RN [2]  
RP SEQUENCE OF 12-158 FROM N.A.  
RC STRAIN=129/SV; TISSUE=T-cell;  
RX MEDLINE=96194901; PubMed=8654948;  
RA Yao Z., Timour M., Painter S., Fanslow W., Spriggs M.K.;  
RT "Complete nucleotide sequence of the mouse CTLA8 gene.";  
RL Gene 168:223-225(1996).  
CC -1- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND HEMATOPOIETIC CYTOKINES (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- TISSUE SPECIFICITY: RESTRICTED TO A SUBSET OF ACTIVATED T-CELLS.  
CC -1- SIMILARITY: BELONGS TO THE IL-17 FAMILY.  
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CC -----  
DR EMBL; U43088; AAB05222.1; -;  
DR EMBL; U35108; AAA93253.1; -;  
DR MGD; MGI:107364; 1117.  
KW Cytokine; Glycoprotein; T-cell; Antigen; Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 26 158 INTERLEUKIN-17.  
FT DISULFID 97 147 BY SIMILARITY.

FT DISULFID 102 149 BY SIMILARITY.  
FT CARBOHYD 71 71 N-LINKED (GLCNAC...)(POTENTIAL).  
SQ SEQUENCE 158 AA: 17490 MW: 3505CL43435FA653 CRC64;

Query Match 13.8%; Score 148.5; DB 1; Length 158;  
Best Local Similarity 37.6%; Pred. No. 3.6e-07;  
Matches 38; Conservative 13; Mismatches 35; Indels 15; Gaps 3;

OY 92 REEVELEADTHORSISPMWRVYDTEDEDRYPQKLAFAECRCICIDARTGRETAALNSVLL 151  
DB 65 RPSDYL-----NRSTSPMTLSRNEDEPDRPSYIWEAQCRHRCVNAE-GKLDHNNNSVLI 118  
OY 152 LQSLYLRRRPPCSRDGSGLPFGAFHFEFIHVPVGCCTV 192  
DB 119 QOEIILVKREPS-----CPTFVEKMLVGVCCTCV 150

RESULT 12  
HNF6\_HUMAN STANDARD: PRT; 465 AA.

AC Q9UBC0; Q9UMR6; Q9744;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).  
GN ONEUT1 OR HNF6A OR HNF6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Furuta H., Horikawa Y., Wang Y.-Q., Bell G.I.;  
RT "Isolation and characterization of the human hepatocyte nuclear factor 6 gene.";  
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Furuta H., Wang Y.-Q., Bell G.I.;  
RT "The sequence of human mRNA for the hepatocyte nuclear factor-6 alpha.";  
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 1-368 FROM N.A., AND VARIANT ALA-75.  
RX MEDLINE=99420592; PubMed=10491763;  
RA Moeller A.M., Ek J., Durvieux S.M., Urhammer S.A., Clausen J.O., Elberg H., Hansen T., Rousseau G.G., Lemaigre F.P., Pedersen O.;  
RT "Hepatocyte nuclear factor-6: associations between genetic variability and type II diabetes and between genetic variability and estimates of insulin secretion.";  
RL Diabetologia 42:1011-1016(1999).  
RN [4]  
RP SEQUENCE OF 174-465 FROM N.A.  
RA Samadani U., Costa R.H.;  
RT "Yeast one-hybrid cloning of the partial human cDNA for hepatocyte nuclear factor 6.";  
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE 5'-DHATTGATATGWD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION.  
CC -1- SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER; LOWER EXPRESSION IN TESTIS AND SKIN.  
CC -1- SIMILARITY: CONTAINS 1 CUT DOMAIN.  
CC -1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.

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CC EMBL: AF035581; AAD02033.1;  
 CC EMBL: AF035580; AAD02033.1; JOINED.  
 DR EMBL: U96173; AAD00826.1;  
 DR EMBL: Y17739; CAB50769.1;  
 DR EMBL: U77975; AAB61705.1;  
 DR TRANSFAC: T03286;  
 DR MIM: 604164;  
 DR InterPro: IPR003350; CUT.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF002376; CUT; 1.  
 DR Pfam: PF00046; homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; FALSE\_NEG.  
 DR PROSITE: PS00071; HOMEBOX\_2; 1.  
 KW Transcription regulation; Homeobox; DNA-binding; Nuclear protein;  
 KW Activator; Polymorphism.  
 FT DNA\_BIND 283 369 CUT.  
 FT DOMAIN 385 444 HOMEBOX.  
 FT DOMAIN 69 72 POLY-HIS.  
 FT DOMAIN 124 138 POLY-HIS.  
 FT DOMAIN 455 460 POLY-SER.  
 FT VARIANT 75 75 P->A.  
 FT CONFLICT 220 220 /FTID=VAR\_010729.  
 FT CONFLICT 284 284 A->T (IN REF. 3 AND 4).  
 FT CONFLICT 288 288 S->N (IN REF. 4).  
 FT CONFLICT 318 318 Q->H (IN REF. 4).  
 FT CONFLICT 386 386 R->K (IN REF. 4).  
 FT CONFLICT 386 386 K->O (IN REF. 4).  
 SQ SEQUENCE 465 AA; 51023 MW; F47F78957A6CF02 CRC64;

Query Match  
 Best Local Similarity 8.0%; Score 85.5; DB 1; Length 465;  
 Matches 48; Conservative 14; Mismatches 53; Indels 71; Gaps 11;

QY 18 AHHPDSLGRHPSHGTPTCYSAEPLIGQAPP-----HLARAKKQCALPVAVSSLEA 72  
 DB 220 AHHPAMLCRHHGQHILTP--TSAGVPIPLGPPHHPHALLNQG--HGQLLGA----- 268  
 QY 73 ASHGRHHERPSAT-----TQCPVLRPEVLEADTHORSISPMRYRVDTDEDRY-- 120  
 DB 269 -----REPNPVYGAOVNSGNSGOMEINRKEVAO-----RITTELKRYSI 310  
 QY 121 POKLAFACICLR--GCID-----ARTGRETALNSVRL-----LOSILVLR 159  
 DB 311 POKLAFACICLR--GCID-----ARTGRETALNSVRL-----LOSILVLR 159  
 QY 160 RRPCSR 165  
 DB 367 LAACKR 372

RESULT 13  
 HNF6\_MOUSE  
 ID HNF6\_MOUSE STANDARD; PRT; 465 AA.  
 AC 008755;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).  
 GN ONECT1 OR HNF6A OR HNF6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Samadani U., Rausa F., Costa R.H.;  
 RT "Mouse hepatocyte nuclear factor-6 cDNA.";

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1 FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE  
 CC 5'-DHATGATGATWMD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE  
 CC OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION (BY  
 CC SIMILARITY).  
 CC -1 SUBUNIT: BINDS DNA AS A MONOMER (BY SIMILARITY).  
 CC -1 SUBCELLULAR LOCATION: Nuclear.  
 CC -1 SIMILARITY: CONTAINS 1 CUT DOMAIN.  
 CC -1 SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: U95945; AAB53863.1;  
 DR TRANSFAC: T03296;  
 DR MGD: MGI:1196423; Onecut1.  
 DR InterPro: IPR003350; CUT.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF02376; CUT; 1.  
 DR Pfam: PF00046; homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; FALSE\_NEG.  
 DR PROSITE: PS00071; HOMEBOX\_2; 1.  
 KW Transcription regulation; Homeobox; DNA-binding; Nuclear protein;  
 KW Activator.  
 FT DNA\_BIND 283 369 CUT.  
 FT DOMAIN 385 444 HOMEBOX.  
 FT DOMAIN 69 72 POLY-HIS.  
 FT DOMAIN 124 138 POLY-HIS.  
 FT DOMAIN 450 460 POLY-SER.  
 SQ SEQUENCE 465 AA; 50952 MW; A770D27DD5AAC896 CRC64;

Query Match  
 Best Local Similarity 8.0%; Score 85.5; DB 1; Length 465;  
 Matches 48; Conservative 14; Mismatches 53; Indels 71; Gaps 11;

QY 18 AHHPDSLGRHPSHGTPTCYSAEPLIGQAPP-----HLARAKKQCALPVAVSSLEA 72  
 DB 220 AHHPAMLCRHHGQHILTP--TSAGVPIPLGPPHHPHALLNQG--HGQLLGA----- 268  
 QY 73 ASHGRHHERPSAT-----TQCPVLRPEVLEADTHORSISPMRYRVDTDEDRY-- 120  
 DB 269 -----REPNPVYGAOVNSGNSGOMEINRKEVAO-----RITTELKRYSI 310  
 QY 121 POKLAFACICLR--GCID-----ARTGRETALNSVRL-----LOSILVLR 159  
 DB 311 POKLAFACICLR--GCID-----ARTGRETALNSVRL-----LOSILVLR 159  
 QY 160 RRPCSR 165  
 DB 367 LAACKR 372

RESULT 14  
 HNF6\_RAT  
 ID HNF6\_RAT STANDARD; PRT; 465 AA.  
 AC P70512; 088755;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Hepatocyte nuclear factor 6 (HNF-6) (One cut domain family member 1).  
 GN ONECT1 OR HNF6A OR HNF6.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;  
 RX MEDLINE=96382488; PubMed=8790352;  
 RA Lemaigre F.P., Durvieux S.M., Truong O., Lannoy V.J., Hsuan J.J.,  
 RA Rousseau G.G.,  
 RT "Hepatocyte nuclear factor 6, a transcription factor that contains a  
 RT novel type of homeodomain and a single cut domain";  
 RT Proc. Natl. Acad. Sci. U.S.A. 93:9460-9464(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM BETA).  
 RC STRAIN-WISTAR;  
 RX MEDLINE=98256275; PubMed=9593691;  
 RA Lannoy V.J., Bueglin T.R., Rousseau G.G., Lemaigre F.P.;  
 RT "Isoforms of hepatocyte nuclear factor-6 differ in DNA-binding  
 RT properties, contain a bifunctional homeodomain, and define the new  
 RT ONECUT class of homeodomain proteins";  
 RT J. Biol. Chem. 273:13552-13562(1998).  
 RN [3]  
 RP CHARACTERIZATION.  
 RX MEDLINE=97042457; PubMed=8887657;  
 RA Samadani U., Costa R.H.;  
 RT "The transcriptional activator hepatocyte nuclear factor 6 regulates  
 RT liver gene expression";  
 RT Mol. Cell. Biol. 16:6273-6284(1996).  
 CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS THE CONSENSUS SEQUENCE  
 CC 5'-DHAAATGATGATWD-3' ON A VARIETY OF GENE PROMOTERS SUCH AS THOSE  
 CC OF HNF3B AND TTR. IMPORTANT FOR LIVER GENES TRANSCRIPTION. THE  
 CC AFFINITY OF HNF-6ALPHA AND HNF-6BETA FOR DNA DIFFERS DEPENDING ON  
 CC THE TARGET SEQUENCE.  
 CC -1- SUBUNIT: BINDS DNA AS A MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN, SPLEEN AND TESTIS.  
 CC -1- SIMILARITY: CONTAINS 1 CUT DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE CUT FAMILY OF HOMEBOX PROTEINS.  
 CC CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: Y96553; CAA65389.1; -  
 CC EMBL: Y14933; CAA75150.1; -  
 CC TRANSEFAC: T03257; -  
 CC DR TRANSFAC: T03258; -  
 CC DR InterPro: IPR003350; CUT.  
 CC DR InterPro: IPR001356; Homeobox.  
 CC DR Pfam: PF02376; CUT; 1.  
 CC DR Pfam: PF00046; homeobox; 1.  
 CC DR SMART: SM00389; HOX; 1.  
 CC DR PROSITE: PS00027; HOMEBOX\_1; FALSE\_NEG.  
 CC DR PROSITE: PS50071; HOMEBOX\_2; 1.  
 CC KW Transcription regulation; Homeobox; DNA-binding; Nuclear protein;  
 CC Activator; Alternative splicing.  
 CC FT DNA\_BIND 283 369 CUT.  
 CC FT DNA\_BIND 385 444 HOMEBOX.  
 CC FT DOMAIN 69 72 POLY-HIS.  
 CC FT DOMAIN 124 138 POLY-HIS.  
 CC FT DOMAIN 455 460 POLY-SER.  
 CC FT VARSPLIC 368 368 A -> AESAMGSGVPSLRITSSGPGQSLVPPPL (IN  
 CC ISOFORM BETA).  
 CC SQ SEQUENCE 465 AA; 51067 MW; BD651267FD7AC896 CRC64;

Query Match 8.0%; Score 85.5; DB 1; Length 465;  
 Best Local Similarity 25.8%; Pred. No. 1;  
 Matches 48; Conservative 14; Mismatches 53; Indels 71; Gaps 11;

18 AHNDPSLGRHSHGTPHCYSAEELPLGQAP-----HLLARAGAKWGQALPALVALVSSLEA 72

DB 220 AHPALGRRHGECHLTP--TSAGMVPINGLPPIHPAHILNAG--HGQLLGTA----- 268  
 OY 73 ASHRGHEHPSAT-----TQCPVLREPEVLEADTHQHSISWRVRVTDDERY-- 120  
 DB 269 -----REPSPVYGAQAVSNGMSGNGMEINTKEVAD-----RITTELRYSI 310  
 OY 121 POKLAFECICR--GCID-----ARTGRTAALNSVRL-----LQSLIVLR 159  
 DB 311 PQALFQVRVLCRSQGLTSLDLRNPVKMSKLSKREIFR----RMMKWLOEPEQRMSALR 366  
 OY 160 RPECNR 165  
 DB 367 LAACKR 372  
 RESULT 15  
 BRM\_DROME  
 ID BRM\_DROME STANDARD; PRT; 1638 AA.  
 AC P25439; Q9VUM5; Q9VUM6;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Homeotic gene regulator (Brahma protein).  
 GN BRM OR CG5942 OR CG18438.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydriodea; Drosophilidae; Drosophila.  
 OX NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RX MEDLINE=92154670; PubMed=1346755;  
 RA Tamkun J.W., Deuring R., Scott M.P., Kissinger M., Pattatucci A.M.,  
 RA Kaufman T.C., Kennison J.A.;  
 RT "Brahma: a regulator of Drosophila homeotic genes structurally  
 RT related to the yeast transcriptional activator SNF2/SWI2";  
 RT Cell 68:561-572(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceoliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champs M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris G., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murthy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paciel J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu K., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: MAY ACT AS COACTIVATOR, ASSISTING ONE OR MORE DEDICATED  
 CC TRANSCRIPTIONAL ACTIVATORS OF ANT-C AND BX-C HOMEOTIC GENES. CAN  
 CC COUNTERACT THE REPRESSIVE EFFECT OF POLYCOMB PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
 CC SHORT FORM, MAY BE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- DEVELOPMENTAL STAGE: HIGHEST EXPRESSION IN UNFERTILIZED EGGS AND  
 CC EARLY EMBRYOS.  
 CC -1- MISCELLANEOUS: 'BRAHMA' MEANS 'FATE' IN INDIA.  
 CC -1- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M85049; AAA19661.1;  
 DR EMBL: AE003529; AAF49557.1;  
 DR EMBL: AE003529; AAF49558.2;  
 DR PIR: A42091; A42091.  
 DR FLYBASE: FBgn00000212; brm.  
 DR InterPro: IPR001487; Bromodomain.  
 DR InterPro: IPR001410; DEAD.  
 DR InterPro: IPR001650; Helicase\_C.  
 DR InterPro: IPR000330; SNF2\_N.  
 DR Pfam: PF00439; bromodomain; 1.  
 DR Pfam: PF00271; helicase\_C; 1.  
 DR Pfam: PF00176; SNF2\_N; 1.  
 DR PRINTS: PR00503; BROMODOMAIN.  
 DR SMART: SM00297; BROMO; 1.  
 DR SMART: SM00487; DEXDC; 1.  
 DR SMART: SM00490; HELIC; 1.  
 DR PROSITE: PS00633; BROMODOMAIN.1; 1.  
 DR PROSITE: PS50014; BROMODOMAIN.2; 1.  
 KW Developmental protein; Transcription regulation; Nuclear protein;  
 KW Activator; Bromodomain; Helicase; ATP-binding; Alternative splicing.  
 FT DOMAIN 201 390 GLN/PRO-RICH.  
 FT NP-BIND 798 805 ATP (POTENTIAL).  
 FT SITE 900 903 DECH BOX.  
 FT DOMAIN 1385 1392 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 1394 1404 ARG/LYS-RICH (BASIC).  
 FT DOMAIN 1405 1410 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 1415 1432 ARG/LYS-RICH (BASIC).  
 FT DOMAIN 1443 1513 BROMODOMAIN.  
 FT DOMAIN 1631 1638 POLY-ASP.  
 FT VARSPIC 121 121 G -> A (IN SHORT ISOFORM).  
 FT VARSPIC 122 222 MISSING (IN SHORT ISOFORM).  
 FT CONFLICT 687 687 D -> Y (IN REF. 1).  
 SO SEQUENCE 1638 AA; 185086 MW; AA494B29F4FE2A4A CRC64;

Query Match 7.9%; Score 84.5; DB 1; Length 1638;  
 Best Local Similarity 22.2%; Pred. No. 5.2; Mismatches 26; Indels 51; Gaps 8;

OY 22 PSIRGPHSHGTHCYSAEPLPGQAPH---LLARGAKWGQALFVALVSSLEAASHNG 77  
 DB 52 PGAYIGHPMOAGPP---GGCPGHMPPHMOGMSKSGPMGMOMP---PTGPNMSPYQT 104  
 OY 78 RHREPSATTOCCPVLR-----PEEVLVDTH--QRSISPMWRVYVTDSDRYPOKIA 125  
 DB 105 HGMPFNAPTOPCIVSPGPGPGPPRERSQENLHALQALRAIDSMERKGLQEDPRYSQILA 164

OY 126 FAECICRCGICDARTGRTAALNSVRLLOS-----LVLRPRPCCSRD----- 166  
 DB 165 -----MRATSKHQLNGNNGVNLRTQTLTAVRLLARNKPIISMQNALQAAGQPP 215  
 OY 167 GSGJLTPGA 175  
 DB 216 GPPIGPPGA 224

Search completed: September 4, 2002, 01:59:50  
 Job time: 187 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 01:55:48 : Search time 23.77 Seconds  
(without alignments)  
1433.740 Million cell updates/sec

Title: US-09-854-280-3  
Perfect score: 1073  
Sequence: 1 MTLPLGLFTWLTHTCLAHN.....FHTFEIHVPVGCCTVLPKRV 197

Scoring table:  
Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: SP\_ARCHAEA:\*
- 2: SP\_BACTERIA:\*
- 3: SP\_FUNGI:\*
- 4: SP\_HUMAN:\*
- 5: SP\_INVERTEBRATE:\*
- 6: SP\_MAMMAL:\*
- 7: SP\_MHC:\*
- 8: SP\_ORGANELLE:\*
- 9: SP\_PHAGE:\*
- 10: SP\_PLANT:\*
- 11: SP\_TODENT:\*
- 12: SP\_VIRUS:\*
- 13: SP\_VERTEBRATE:\*
- 14: SP\_UNCLASSIFIED:\*
- 15: SP\_VIRUS:\*
- 16: SP\_BACTERIAP:\*
- 17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073	100.0	197	4	Q9POM4
2	1065	99.3	197	4	Q9HC75
3	173	16.1	109	4	Q96P18
4	173	16.1	163	4	Q96PD4
5	169.5	15.8	180	11	Q99MY3
6	168.5	15.7	180	11	Q9QXR6
7	165.5	15.4	177	4	Q9H293
8	160.5	15.0	215	11	Q9CT14
9	157.5	14.7	151	12	Q40633
10	157.5	14.7	178	11	Q9E016
11	157	14.6	141	6	Q9E156
12	154.5	14.4	180	4	Q9UHE5
13	136	12.7	78	4	Q9NUE6
14	129.5	12.1	111	11	Q9E017
15	110	10.3	148	5	Q19778
16	95.5	8.9	93	6	Q9BEH5

17	89.5	8.3	168	2	Q9XDC3	Q9XDC3 herbaspiril
18	89.5	8.3	521	12	Q9DP52	Q9DP52 melegrid h
19	88.5	8.2	521	12	Q9E1H8	Q9E1H8 melegrid h
20	88	8.2	1548	4	Q9MYW9	Q9MYW9 homo sapien
21	88	8.2	2161	4	Q9T566	Q9T566 homo sapien
22	86.5	8.1	389	10	Q9LE01	Q9LE01 arabisdopsis
23	86	8.0	297	2	Q99391	Q99391 streptomyc
24	86	8.0	1098	11	Q9JL71	Q9JL71 mus musculu
25	84.5	7.9	317	4	Q9RTV9	Q9RTV9 homo sapien
26	84	7.8	179	10	Q93Z24	Q93Z24 arabisdopsis
27	84	7.8	354	10	Q9SE51	Q9SE51 arabisdopsis
28	82	7.6	413	3	Q9P795	Q9P795 schizosach
29	82	7.6	415	3	Q9LG13	Q9LG13 oryza sativ
30	81.5	7.6	306	2	Q9LAD4	Q9LAD4 xanthomonas
31	81.5	7.6	380	5	Q9G5Z8	Q9G5Z8 caenorhabdi
32	81	7.5	553	16	Q9T1783	Q9T1783 pseudomonas
33	80.5	7.5	283	5	Q9W4E1	Q9W4E1 dirosophila
34	80.5	7.5	358	5	Q9U123	Q9U123 leishmania
35	80.5	7.5	638	4	Q96LD4	Q96LD4 homo sapien
36	80	7.5	408	4	Q96H86	Q96H86 homo sapien
37	80	7.5	411	16	Q96313	Q96313 mycobacteri
38	79.5	7.4	681	5	Q9SRM4	Q9SRM4 dirosophila
39	79.5	7.4	745	13	Q98S05	Q98S05 brachydanio
40	79.5	7.4	1406	5	Q9V4D4	Q9V4D4 dirosophila
41	79.5	7.4	1406	5	Q9U110	Q9U110 dirosophila
42	79.5	7.4	1408	5	Q9XZU7	Q9XZU7 dirosophila
43	79	7.4	465	4	Q9BMD7	Q9BMD7 homo sapien
44	79	7.4	837	4	Q9Y4R8	Q9Y4R8 homo sapien
45	79	7.4	837	4	Q9BR21	Q9BR21 homo sapien

# ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	197 AA.
ID	Q9POM4			
AC	Q9POM4	01-OCT-2000 (TREMBL)	15, Created	
DT	01-OCT-2000 (TREMBL)	15, Last sequence update		
DE	01-OCT-2000 (TREMBL)	15, Last annotation update		
DR	INTERLEUKIN 17C.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
NCBI_TaxID	9606;			
NCBI	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-20105548; PubMed-10639155;			
RA	Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,			
RT	Gurney A.L., Wood W.L.;			
RT	"Cloning and Characterization of IL-17B and IL17C, Two New Members of			
RT	the IL-17 Cytokine Family."			
RT	Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).			
DR	EMBL: AF152099; AAF28105.1;			
SQ	SEQUENCE 197 AA; 21765 MW; BAE0132E18DE7D08 CRC64;			

Query Match	100.0%;	Score 1073;	DB 4;	Length 197;
Best Local Similarity	100.0%;	Pred. No. 2.1e-100;		
Matches 197;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	MTLPLGLFTWLTHTCLAHNPSLRHPSHGTPHCYSAEELPLGAPPHLLARGLKWKQ	60	
DB	1	MTLPLGLFTWLTHTCLAHNPSLRHPSHGTPHCYSAEELPLGAPPHLLARGLKWKQ	60	
QY	61	ALPVALVSSLEAASHRGHRRSPATTCVLRPEEVLADTQRSTSPWRYVDVDEDEY	120	
DB	61	ALPVALVSSLEAASHRGHRRSPATTCVLRPEEVLADTQRSTSPWRYVDVDEDEY	120	
QY	121	PKLAFAECLRCGICDARTGTRETALNSVRLQLSLVLRPPCSRDGSLPPGAFAPFT	180	
DB	121	PKLAFAECLRCGICDARTGTRETALNSVRLQLSLVLRPPCSRDGSLPPGAFAPFT	180	

OY 181 EFTHVPGCTCVPRLSV 197  
 DB 181 EFTHVPGCTCVPRLSV 197

## RESULT 2

ID 09HC75 PRELIMINARY; PRT; 197 AA.

AC 09HC75; 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang W., He L., Wan T., Yuan Z., Cao X.;  
 RT "Novel human cytokine CX2 with homology to IL-17,"  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF142410; AAC27921.1;  
 SQ SEQUENCE 197 AA; 21784 MW; BAFBBA9F6314A768 CRC64;

Query Match 99.3%; Score 1065; DB 4; Length 197;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-99;  
 Matches 196; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MTLPLGLFLFWLHLCIAHNDPSLRGPHSHGTPHCYAEELPLGQAPPHILANGAKWQ 60  
 DB 1 MTLPLGLFLFWLHLCIAHNDPSLRGPHSHGTPHCYAEELPLGQAPPHILANGAKWQ 60  
 OY 61 ALPVALVSLAASHRGHRRPSTATQCPVLRPEVELEADTHORSISPMWRVDTDDRY 120  
 DB 61 ALPVALVSLAASHRGHRRPSTATQCPVLRPEVELEADTHORSISPMWRVDTDDRY 120  
 OY 121 POKLAFACLCRGCTDARTGRTAALNSVRLQSLILVLRPPCRDGGSLPTGAFAFHT 180  
 DB 121 POKLAFACLCRGCTDARTGRTAALNSVRLQSLILVLRPPCRDGGSLPTGAFAFHT 180  
 OY 181 EFTHVPGCTCVPRLSV 197  
 DB 181 EFTHVPGCTCVPRLSV 197

## RESULT 3

ID 096P18 PRELIMINARY; PRT; 109 AA.

AC 096P18; 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21475866; PubMed=11591768;  
 RA Kawaguchi M., Onouchi L.F., Li X.-D., Essayan D.M., Schroeder J.,  
 RT "Identification of a Novel Cytokine, ML-1, and Its Expression in  
 RT Subjects with Asthma,"  
 RL J. Immunol. 167:4430-4435(2001).  
 DR EMBL; AF332389; AAL14427.1;  
 SQ SEQUENCE 109 AA; 12327 MW; 52C5B34C36DC30EB CRC64;

Query Match 16.1%; Score 173; DB 4; Length 109;

Best Local Similarity 39.0%; Pred. No. 5.7e-10;  
 Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

OY 97 LEADTHORSISPMWRVDTDDRYPOKLAFAELCRGCTDARTGRTAALNSVRLQSL 156  
 DB 16 MSRNIESRSTSPMNTYVTWDPNRPSEVVOACRNLGCTINQ-GKEDISMSNVPIQOETL 74

OY 157 VLRR--PCSRDGSGLPTGAFAFHTEFIHVPVGTCTVP 194  
 DB 75 VVRRKHGCS-----VSFOLEKVLVTGCTCTVP 103

## RESULT 4

ID 096PD4 PRELIMINARY; PRT; 163 AA.

AC 096PD4; 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=21475830; PubMed=11591732;  
 RA Starnes T., Robertson M.J., Sledge G., Kelich S., Nakshatri H.,  
 RA Broxmeyer H.E., Thomas R.;  
 RT "Cutting Edge: IL-17F, a novel cytokine selectively expressed in  
 RT activated T cells and monocytes, regulates angiogenesis and  
 RT endothelial cell cytokine production,"  
 RL J. Immunol. 167:4137-4140(2001).  
 DR EMBL; AF384857; AAK83350.1;  
 SQ SEQUENCE 163 AA; 18045 MW; E5287737C9E7BD46 CRC64;

Query Match 16.1%; Score 173; DB 4; Length 163;  
 Best Local Similarity 39.0%; Pred. No. 8.9e-10;  
 Matches 39; Conservative 16; Mismatches 31; Indels 14; Gaps 3;

OY 97 LEADTHORSISPMWRVDTDDRYPOKLAFAELCRGCTDARTGRTAALNSVRLQSL 156  
 DB 70 MSRNIESRSTSPMNTYVTWDPNRPSEVVOACRNLGCTINQ-GKEDISMSNVPIQOETL 128  
 OY 157 VLRR--PCSRDGSGLPTGAFAFHTEFIHVPVGTCTVP 194  
 DB 129 VVRRKHGCS-----VSFOLEKVLVTGCTCTVP 157

## RESULT 5

ID 099MY3 PRELIMINARY; PRT; 180 AA.

AC 099MY3; 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=BAIB/C;  
 RA Zhang W., Cao X.;  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF250308; AAK37427.1;  
 SQ SEQUENCE 180 AA; 20268 MW; AAEACF5FACA3D11E CRC64;

Query Match 15.8%; Score 169.5; DB 11; Length 180;



Best Local Similarity 27.0%; Pred. No. 2.2e-09;  
Matches 53; Conservative 28; Mismatches 82; Indels 33; Gaps 6;

OY 7 LFLFLMLHLCIA-HHDPSPRGHPSHGTPHCYSAEPLPGQAPPHILLAGAKWGAALPVA 65  
DB 7 LFLFLAISIFLAPSHRNKGRKGGKPS-----PLAPGP-----HOVPLD 48  
OY 66 LVSSLEASHRGHRSPTATOCVPLRPEVLEAD-----THORSISPMRYRVPTD 116  
DB 49 LVSRKAPVYRMEYERTLGEVMAQLANSEPPAKKCEVNLQMLSKRSLSPMGISIND 108  
OY 117 EDYRPOKLAFAECLRCGCIIDARTGRTALNSVRLQSLVLRRCPSRSGSLPTPGAF 176  
DB 109 PSRIADLPKARCLICGCVNPFMDRSMVSVPVF-SQVPRRRRLCPGP-----PRGPC 163  
OY 177 AFHTERIHVPVGTCTV 192  
DB 164 RORVYMETIAGCTCT 179

# RESULT 6

O9QXT6 PRELIMINARY; PRT; 180 AA.  
AC O9QXT6;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TREMBLrel. 17, Last annotation update)  
DE CYTOKINE-LIKE PROTEIN ZCYT07 (NEURONAL INTERLEUKIN-17 RELATED FACTOR)  
DE (INTERLEUKIN 17b).  
GN IL17B OR ZCYT07.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN 11  
RP SEQUENCE FROM N.A.  
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,  
RA Martinez T., Hoffman R., O'Hara P.;  
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
RN 12  
RP SEQUENCE FROM N.A.  
RA Moore E.E., Presnell S., Garrigues U., Guilbot A., Leguern E.,  
RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;  
RT "Identification of a novel IL-17 related factor: demonstration of  
RT neuronal expression and evaluation as a candidate for the chromosome  
RT 5q-linked form of Charcot-Marie-Tooth disease."  
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
RN 13  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AF184970; AAF01319.1;  
DR EMBL; AF218726; AAG4135.1;  
DR EMBL; BC002271; AAH02271.1;  
DR MGD; MGI:1928397; 1117b.  
SQ SEQUENCE 180 AA; 20309 MW; E26F4C72001997C5 CRC64;

Query Match 15.7%; Score 168.5; DB 11; Length 180;  
Best Local Similarity 27.0%; Pred. No. 2.8e-09;  
Matches 53; Conservative 28; Mismatches 82; Indels 33; Gaps 6;

OY 7 LFLFLMLHLCIA-HHDPSPRGHPSHGTPHCYSAEPLPGQAPPHILLAGAKWGAALPVA 65  
DB 7 LFLFLAISIFLAPSHRNKGRKGGKPS-----PLAPGP-----HOVPLD 48  
OY 66 LVSSLEASHRGHRSPTATOCVPLRPEVLEAD-----THORSISPMRYRVPTD 116  
DB 49 LVSRKAPVYRMEYERTLGEVMAQLANSEPPAKKCEVNLQMLSKRSLSPMGISIND 108  
OY 117 EDYRPOKLAFAECLRCGCIIDARTGRTALNSVRLQSLVLRRCPSRSGSLPTPGAF 176  
DB 109 PSRIADLPKARCLICGCVNPFMDRSMVSVPVF-SQVPRRRRLCPGP-----PRGPC 163

OY 177 AFHTERIHVPVGTCTV 192  
DB 164 RORVYMETIAGCTCT 179

# RESULT 7

O9H293 PRELIMINARY; PRT; 177 AA.  
AC O9H293;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE INTERLEUKIN 17E.  
GN IL17E.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN 11  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21125711; PubMed=11058597;  
RA Lee J., Ho W.-H., Maruoka M., Corpuz R.T., Baldwin D.T., Foster J.S.,  
RA Goddard A.D., Yansura D.G., Vandlen R.L., Wood W.I., Gurney A.L.;  
RT "IL-17E, a Novel Proinflammatory Ligand for the IL-17 Receptor Homolog  
RT IL-17R1".  
RL J. Biol. Chem. 276:1660-1664(2001).  
DR EMBL; AF305200; AAG40848.1;  
SQ SEQUENCE 177 AA; 20330 MW; 52D895710CD59871 CRC64;

Query Match 15.4%; Score 165.5; DB 4; Length 177;  
Best Local Similarity 29.7%; Pred. No. 5.5e-09;  
Matches 52; Conservative 16; Mismatches 70; Indels 37; Gaps 7;

OY 27 HPHSHGTPHCYS-----AEELPLGQAPPHILLAGAKWGAALVSSLEASHRGHRR 81  
DB 31 HRYSHMPSCCPKSGQGTSEL-----LRW-STVP---VPLEPARPNHPPS 73  
OY 82 PSATTCVPLRPEVLEADTHORSISPMRYRVPTDDEDRIPKLAFAECLRCGCIIDART 141  
DB 74 CRASEDGPV-----NSRAISPMRYEELDRDINRLPDLIYHARCICPHCVSLQTS 122  
OY 142 ETAL-NSVRLQSLVLRRCPSRSGSLPTPGAFAFHTERIHVPVGTCTVPR 195  
DB 123 HMDPGENSELYHNQTVYRRPCHEKG---THKGICLERRLRYSLACVYRPR 174

# RESULT 8

O9CT14 PRELIMINARY; PRT; 215 AA.  
AC O9CT14;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE 111006016R1K PROTEIN (FRAGMENT).  
GN IL17B OR 111006016R1K.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN 11  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaio I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gastlisch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monden P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whittaker C., Wilming L.,  
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RA Functional annotation of a full-length mouse cDNA collection."  
 RL NATURE 409:685-690(2001).  
 DR EMBL AK003506; BAB2826.1;  
 DR MGD; MG1:1928397; 1117b.  
 FT NON\_TER  
 SO SEQUENCE 215 AA; 24196 MW; 21468E7E01A92154 CRC64;

Query Match 15.0%; Score 160.5; DB 11; Length 215;  
 Best Local Similarity 29.8%; Pred. No. 2; 2e-08;  
 Matches 48; Conservative 25; Mismatches 63; Indels 25; Gaps 5;

QY 45 GOAPPHILGAKWGALPVALVSSLEASHRGHHER-----PSATGCPVL 91  
 DB 66 GQRRPPLAGP---HOVPLDLYSRVAPYARMERYENLGEVVAQLRNISEPAKRCCEV- 121  
 QY 92 RPEVLEADYHORSISFWRVDTDEDRYPOKLAFAECRCGIDARTGETALNSVRL 151  
 DB 122 ---NLQMLSNKRSLSWGSINHDPSRIPADLPEARCLGCVNPTTMDNSMSVFPV 178  
 QY 152 LQSLVLRPPCSRDGSGLPFGAFHTEFIHVPVGCCTV 192  
 DB 179 F-SQVPRRLCP---PRGPCRRVYMETIIVAGCTCI 214

RESULT 9  
 ID 040633 PRELIMINARY; PRT; 151 AA.  
 AC 040633;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE INTERLEUKIN 17.  
 GN ORE13.  
 OS Salimline herpesvirus 2.  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Gamaherpesvirinae; Rhadinovirus.  
 OX NCBI\_TaxID=10381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C-488;  
 RX MEDLINE=98037620; PubMed=9371569;  
 RA Knappe A., Hiller C., Thura M., Wittmann S., Hofmann H.,  
 RA Fleckenstein B., Fickenscher H.;  
 RT "The superantigen-homologous viral immediate-early gene ie14/vsag 1n  
 herpesvirus salimline-transformed human T cells";  
 RL J. Virol. 71:9124-9133(1997).  
 DR EMBL; Y13183; CAA73627.1;  
 SO SEQUENCE 151 AA; 17189 MW; 49B2C9430C46BE32 CRC64;

Query Match 14.7%; Score 157.5; DB 12; Length 151;  
 Best Local Similarity 28.6%; Pred. No. 3e-08;  
 Matches 46; Conservative 22; Mismatches 58; Indels 35; Gaps 5;

QY 36 CVSAEELPIGQAPPHILGAKWGALPVALVSSLEASHRGHHERPSATGCPVLRPEE 95  
 DB 18 CIYKSTTSNAQPRCLAA-----NNSFPRSVMTLSIRNMNTSSKRAS----- 60  
 QY 96 VLEADYHORSISFWRVDTDEDRYPOKLAFAECRCGIDARTGETALNSVRLQSL 155  
 DB 61 ----DYNNSTSPWTLIRNEDDQDRYPSVIMKACRYLGCYNA-DGVNVDHMSVPIQDEL 115

QY 156 LVLR--RPPCSRDGSGLPFGAFHTEFIHVPVGCCTV 194  
 DB 116 LVVRKGNPCPN-----SFLEKRLVYVGCCTV 145

RESULT 10  
 ID 09E016 PRELIMINARY; PRT; 178 AA.  
 AC 09E016;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE NEURONAL INTERLEUKIN-17 RELATED FACTOR (FRAGMENT).  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 OX NCBI\_TaxID=10036;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Moore E.E., Presnell S., Garrigues U., Guilbot A., Leguern E.,  
 RA Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;  
 RT "Identification of a novel IL-17 related factor: Demonstration of  
 RT neuronal expression and evaluation as a candidate for the chromosome  
 RT 5q-linked form of Charcot-Marie-Tooth disease";  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF218725; AAG44134.1;  
 FT NON\_TER  
 SO SEQUENCE 178 AA; 20071 MW; 03D02D60BEC89A51 CRC64;

Query Match 14.7%; Score 157.5; DB 11; Length 178;  
 Best Local Similarity 29.5%; Pred. No. 3.6e-08;  
 Matches 46; Conservative 23; Mismatches 70; Indels 17; Gaps 4;

QY 45 GOAPPHILGAKWGALPVALVSSLEASHRGHHERPSATGCPVLRPEVLEAD----- 100  
 DB 31 GQVRPPLAGP---HOVPLDLYSRVAPYARMERYENLGEVVAQLRNISEPAKRCCEV 87  
 QY 101 ----THOSISFWRVDTDEDRYPOKLAFAECRCGIDARTGETALNSVRLQSL 155  
 DB 88 LQMLSNKRSLSWGSINHDPSRIPADLPEARCLGCVNPTTMDNSMSVFPV-SO 146  
 QY 156 LVLRPPCSRDGSGLPFGAFHTEFIHVPVGCCTV 191  
 DB 147 VVPRRLCP---PRGPCRRVYMETIIVAGCTC 178

RESULT 11  
 ID 095L56 PRELIMINARY; PRT; 141 AA.  
 AC 095L56;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE INTERLEUKIN 17 (FRAGMENT).  
 GN IL17.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lee I.-K., Mwangi S.M., Olsen S., Kehrli M. Jr.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF416586; AAL08013.1;  
 FT NON\_TER  
 SO SEQUENCE 141 AA; 15945 MW; 94077A79DD803F3E CRC64;

Query Match 14.6%; Score 157; DB 6; Length 141;



RT "Identification of a novel IL-17 related factor: Demonstration of  
 RT neuronal expression and evaluation as a candidate for the chromosome  
 5q-linked form of Charcot-Marie-Tooth disease."  
 RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF218724; AAC44133.1;  
 FT NON TER 1 1  
 FT NON TER 111 111  
 SO SEQUENCE 111 AA; 12628 MW; D1598392981BA867 CRC64;

Query Match 12.1%; Score 129.5; DB 11; Length 111;  
 Best Local Similarity 37.8%; Pred. No. 14e-05;  
 Matches 28; Conservative 16; Mismatches 25; Indels 5; Gaps 2;

QY 101 THORSTISPMRYVDDEDEYPOKLAFAECICGCIIDARTGRTAALNSVRLQSLVLR 160  
 Db 30 SNKRSLSPMGYSINHPSRIPEDLPKARCLCGCVNPFIMQEDRSMSVPEV-SQVPPVR 88  
 QY 161 RPSRDSGLPTPG 174  
 Db 89 RLCFQP---PRPG 98

RESULT 15  
 ID 019778 PRELIMINARY; PRT; 148 AA.  
 AC 019778:  
 DT 01-NOV-1996 (TRENBLrel. 01; Created)  
 DT 01-NOV-1996 (TRENBLrel. 01; Last sequence update).  
 DE 01-DEC-2001 (TRENBLrel. 19; Last annotation update)  
 GN F25D1.3 PROTEIN.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kelly P.F.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL: Z73973; CAA98268.1;  
 SO SEQUENCE 148 AA; 16738 MW; ADB51FA38DFB3940 CRC64;

Query Match 10.3%; Score 110; DB 5; Length 148;  
 Best Local Similarity 33.0%; Pred. No. 0.0018;  
 Matches 31; Conservative 17; Mismatches 34; Indels 12; Gaps 4;

QY 103 QRSISPMRYVDDEDEYPOKLAFAECICGCIIDARTGRTAALNSVRLQSLVLR 162  
 Db 51 ERALCPWDSRVNVOESREPLIAESVLC-----KSRGSGTGAFCMPYVRVPIIRVS 104  
 QY 163 CSRDSGLPTPGAFAPFHTPIHVPVGCCTVLPSS 196  
 Db 105 CDR-STGL--NMYVSTELI TVGCHSVLPRT 132

Search completed: September 4, 2002, 01:59:18  
 Job time: 210 sec